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From: Jiang, Dong  
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Please search SEQ ID NO:3

Priority: 5/14/99  
Chen (Genetech)

-issued

-commercial

no art.

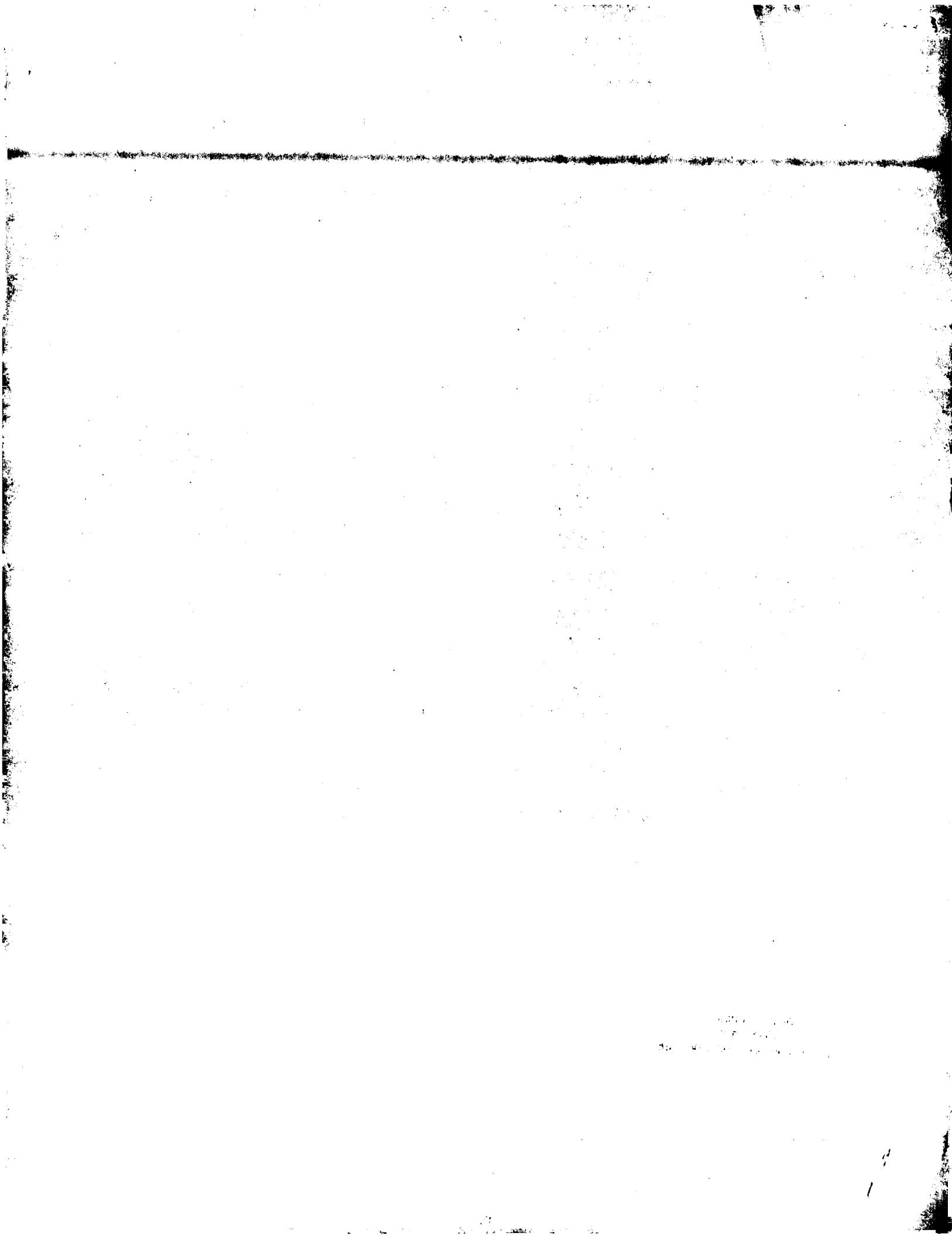
Please send results on paper to Dong Jiang in 10D-08 (mail stop CM1-10D19).  
Thank you very much.

Dong Jiang (78243)  
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U.S. Patent and Trademark Office  
Art Unit 1646  
dong.jiang@uspto.gov  
CM1-10D08  
Mail stop: CM1-10D19

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Date Picked Up: \_\_\_\_\_  
Date Completed: 8/25/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_







Db	121	pqklafaeclrcidartgretaalnsvrllqslvrrpcsdrgsllptpgafafht	180	Db	1	mtllpgllftwlhtciahhhdpsirgshgtphcysaeelpgqapphillargakwgg	60
Qy	181	EFTHVPGCTCVLPRSV	197	Qy	61	ALPVIALSSLEASHRGHERSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDRY	120
Db	181	efihvpvgctcvlpervs	197	Db	61	alpvialssleashrgherpsatqcpvlpervleadthqrsispwryrvtdeyry	120
RESULT	3			Qy	121	PQKLAFAECLCRCIDARTGRETAALNSVRLLOSSLVLRRPPOSRDGSGLPPGAFAFHT	180
	AAB07684			Db	121	pqklafaeclrcidartgretaalnsvrllqslvrrpcsdrgsllptpgafafht	180
ID	AAB07684	standard; Protein;	197 AA.	Qy	181	EFIHVPGCTCVLPRSV	197
XX				Db	181	efihvpvgctcvlpervs	197
AC	AAB07684;			Qy	181	efihvpvgctcvlpervs	197
XX	07-NOV-2000	(first entry)		Db	181	efihvpvgctcvlpervs	197
XX							
DE	A human interleukin-171 polypeptide.						
XX							
KW	Interleukin; IL-171; cytokine; CtnA-8; IL-17; IL-172; IL-173;						
XX	IL-174; IL-176; IL-177; cell proliferation; cancer.						
OS	Homo sapiens.						
XX							
Key	Location/Qualifiers						
PH	1..17						
FT	/note= "signal peptide"						
Protein	18..197						
FT	/note= "mature protein"						
FT	55..57						
Modified-site	/note= "putative glycosylation site"						
XX							
PN	WO200042187-A1.						
XX							
PD	20-JUL-2000.						
XX							
PF	10-JAN-2000; 2000WO-US000005.						
XX							
PR	11-JAN-1999; 99US-0229402.						
XX							
PA	(SCHE ) SCHERRING CORP.						
XX							
PI	Gorman DM, Bazan JF, Kastlein RA;						
XX							
WPI	2000-476060/41.						
DR	N-PSDB; AAA59149.						
XX							
PT	New DNA sequence encoding a mammalian homolog of CTLA-8, designated IL-171 (IL-171), useful for recombinant production of IL-171 which can be used for treating conditions associated with abnormal physiology or development -						
PT	Claim 11; Page 10-11; 111pp; English.						
PS	XX						
CC	The present sequence represents an interleukin (IL)-171 polypeptide. It is a mammalian homologue of the cytokine designated CTLA-8 (also referred to as IL-17). The specific sequence also describes homologues IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA sequence encoding IL-171 is useful for identifying genes, mRNA and cDNA molecules which code for related or homologous proteins. The IL-171 protein, antibodies against IL-171, and compounds which have binding affinity to IL-171 are useful in treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions, or degenerative conditions. The IL-171 protein can be used in kits and assay methods for identifying CC compounds that selectively bind to IL-171.						
CC	XX						
CC	Sequence 197 AA;						
Query Match	100.0%	Score 1073; DB 21; Length 197;					
Best Local Similarity	100.0%	Pred. No. 4..6e-109;					
Matches	197; Conservative 0; Mismatches 0;	Indels 0; Gaps 0;					
Qy	1	MTLLPGLLFTWLHTCLAHHDPSLRLGPHSHGTPHCSAEEELPLGQAPPILLARGAKWGGQ	60				

Query Match	100.0%	Score 1073;	DB 21;	Length 197;	DR	WPI: 2000-116314/10.
Best Local Similarity	100.0%	Pred. No. 4.e-109;	0;	Mismatches 0;	DR	N-PSDB; AAZ29728.
Matches 197;	Conservative	0;	Indels 0;	Gaps 0;	PT	New polypeptides designated PRO1031 and PRO1122 used to treat a
					PT	degenerative cartilaginous disorder
					XX	
Qy	1	MTLPGGLFLPTWLHTCLAHHDPSLRLGRPHSHGTPHCSYSAELPLGQAPPHLARGAKWQ	60	XX	XX	Claim 23; Fig 3; 141pp; English.
Db	1	mtlpgglflptwlhtclahhdpslrlgrphshgtpchcsyaaelplgqapphlargakwq	60	CC	CC	The present sequence is the human PRO1122 polypeptide, also referred to
Qy	61	ALPVAYLSSLEAASHRGHRHERPSATTQCPVLRPEEVLADTHORSISWRYRVDTDEDRY	120	CC	CC	as UNQ561, and as interleukin-17C (IL-17C) encoded by
Db	61	alpvaylssleashrghrherpsattqcpvlrpeevladtorsiswryrvtdey	120	CC	CC	clone DNA62377-1381. This sequence has identity with the
Qy	121	PQKIAFAECCLRCGCIARTGRETAAALNSVRLQSLVIRRPCSRSRDGSGLPTGAFAH	180	CC	CC	cytokine IL-17 and cytotoxic T-lymphocyte-associated antigen 8 (CTLA-8)
Db	121	pqkiafaecclrcgciartgretaaalnsvrlqslvIRRPCSRSRDGSGLPTGAFAH	180	CC	CC	and has leucine zipper pattern. PRO1122 is expressed in pancreas, small
Qy	181	EFTHVPGVCTCVLPLRSV	197	CC	CC	intestine, stomach and testis also. It shares about 26-28% amino acid
Db	181	efthvpgvctcvlplrsv	197	CC	CC	identity with IL-17 and IL-17B. The entire coding region of IL-17C can
Qy	181	EFTHVPGVCTCVLPLRSV	197	CC	CC	be used as hybridisation probe. The PRO1122 polypeptide, agonist or
Db	181	efthvpgvctcvlplrsv	197	CC	CC	antagonist, is used to diagnose and treat a degenerative cartilaginous
Qy	181	EFTHVPGVCTCVLPLRSV	197	XX	XX	disorder.
Db	181	efthvpgvctcvlplrsv	197	SQ	Sequence 197 AA;	
RESULT	5	Query Match	100.0%	Score 1073;	DB 21;	Length 197;
ID	AAV44460	Best Local Similarity	100.0%	Pred. No. 4.e-109;	DR	0;
ID	AAV44460	Matches 197;	Conservative 0;	Mismatches 0;	PT	Gaps 0;
AC	AAV44460;				XX	
XX					XX	
DT	27-MAR-2000	(first entry)			XX	
DE	Human Interleukin 17C, PRO1122 polypeptide.				XX	
DE	Interleukin; IL-17C; PRO1122 polypeptide; clone DNA2377-1381-1; UNQ561;				XX	
KW	cytokine IL-17; cytotoxic T-lymphocyte-associated antigen 8; CTLA-8;				XX	
KW	hybridisation probe; antagonist; degenerative cartilaginous disorder;				XX	
KW	agonist; diagnose; therapy.				XX	
OS	Homo sapiens.				XX	
FH	Key	Location/Qualifiers			XX	
FT	Peptide	1..18			XX	
FT	/label= signal_peptide				XX	
FT	Protein	19..197			XX	
FT	/label= Mature_IL-17C_polypeptide				XX	
FT	/note= "Used to treat degenerative cartilaginous disorder"				XX	
FT	Misc-difference 109				XX	
FT	/note= "Conserved Trp residue"				XX	
FT	Misc-difference 129				XX	
FT	/note= "Conserved Cys residue"				XX	
FT	Misc-difference 134				XX	
FT	/note= "Conserved Cys residue"				XX	
FT	Misc-difference 163				XX	
FT	/note= "Conserved Cys residue"				XX	
FT	Misc-difference 189				XX	
FT	/note= "Conserved Cys residue"				XX	
FT	Misc-difference 191				XX	
FT	/note= "Conserved Cys residue"				XX	
XX	WO960127-A2.				XX	
XX	25-NOV-1999.				XX	
PD					XX	
PF	14-MAY-1999;	99WO-US10733.			XX	
XX					XX	
PR	15-MAY-1998;	98US-0085579.			PR	
PR	23-DEC-1998;	98US-0113621.			PR	
XX					XX	
PA	(GETH ) GENENTECH INC.				PA	
XX					XX	
PI	Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI;				PI	
XX					XX	

RESULT 7  
 AA66121  
 ID AAG66121 standard; Protein; 197 AA.  
 XX  
 AC AAG66121;  
 XX  
 DT 13-MAR-2002 (first entry)  
 XX  
 DE Human interleukin (IL)-21 amino acid sequence.  
 XX  
 KW Interleukin; IL-21; IL-22; immunosuppressive; cytostatic; thrombolytic;  
 KW antiinflammatory; antibacterial; gene therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Location/Qualifiers  
 1..18  
 FT Peptide /note= "signal peptide"  
 19..197  
 FT Protein /note= "mature protein"  
 FT Domain /note= "conserved domain V"  
 63..68  
 FT Domain /note= "conserved domain VI"  
 104..109  
 FT Domain /note= "conserved domain VII"  
 113..121  
 FT Domain /note= "conserved domain I"  
 129..134  
 FT Domain /note= "conserved domain II"  
 156..162  
 FT Domain /note= "conserved domain III"  
 185..192  
 FT Domain /note= "conserved domain IV"  
 XX  
 PN US2001023070-A1.  
 XX  
 PR 2000-072622/06.  
 DR N-PSDB; AAZ36836.  
 XX  
 PT Novel polynucleotides used to develop products for treating e.g. immune  
 PT disorders, blood disorders, autoimmune disorders, allergies,  
 PT inflammation, hyperproliferative disorders or infections  
 XX  
 PR 2000-072622/06.  
 DR N-PSDB; AAZ36836.  
 XX  
 PT The present sequence represents a human interleukin-21 (IL-21)  
 PT protein. The specification also describes IL-22 polynucleotides and  
 CC polyptides. The IL-21 polynucleotide was isolated from a cDNA library  
 CC of apoptotic T-cells. IL-21 and IL-22 may be useful in treating  
 CC deficiencies or disorders of the immune system, by activating or  
 CC inhibiting the proliferation, differentiation, or mobilization of  
 CC immune cells, treating or detecting deficiencies or  
 CC disorders of haematopoietic cells, to modulate haemostatic or  
 CC thrombolytic activity, in treating or detecting autoimmune disorders,  
 CC treating asthma (particularly allergic asthma) or other respiratory  
 CC problems, to treat and/or prevent organ rejection or graft-versus-host  
 CC disease (GVHD), to modulate inflammation, to treat or detect  
 CC hyperproliferative disorders, to treat or detect infectious agents, to  
 CC differentiate, proliferate and attract cells, leading to the  
 CC regeneration of tissues, IL-21 and IL-22 may also increase or decrease  
 CC the differentiation or proliferation of embryonic stem cells and  
 CC haematopoietic lineage, may be used to modulate mammalian  
 CC characteristics.  
 XX  
 SQ Sequence 197 AA;  
 XX  
 P1 Ebner R, Ruben SM;  
 XX  
 DR WPI: 2001-638470/73.  
 N-PSDB; AA167878.  
 XX  
 PT New interleukin-21 and interleukin-22 polynucleotides and polypeptides,  
 PT useful for treating, preventing or diagnosing e.g. disorders of  
 PT hematopoietic cells, autoimmune disorders, or hyperproliferative  
 PT diseases.  
 XX  
 PS Claim 26; Fig 6A-B; 87pp; English.  
 XX  
 DR The invention relates to novel human proteins designated interleukin  
 CC (IL)-21 and IL-22. The IL-21 and IL-22 polynucleotides can be used in  
 CC linkage analysis as a marker for those specific chromosome, in chromosome  
 CC mapping, to control gene expression through triple helix formation or  
 CC antisense DNA or RNA, in gene therapy, in identifying individuals from  
 CC minute biological samples, as an alternative to restriction fragment  
 CC length polymorphism (RFLP) analysis, as polymorphic markers for forensic  
 CC purposes, as molecular weight markers, or as diagnostic probes. IL-21 and  
 CC IL-22 polypeptides can be used to treat, prevent or diagnose diseases of  
 CC the immune system by activating or inhibiting the proliferation,

Query Match 100.0%; Score 1073; DB-21; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 4..6e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLPGLLWLTWCAHDPDSLRGPHSHGTPHCTSAEELPLGQAPPHLARGAKWQ 60  
 Db 1 mtlpgllwltwcahdpdslrghphshgtphtcsaeeplgqapphlargakwq 60

Qy 61 ALPVALYSSLEAASHRQRHERPSATTOCPVLRPEEVLEADTHORSISPVWRYTVDTDEDRY 120  
 Db 61 alpvalysseashrqherpsatccpvrpeevleadtqrsispwrytvdtddry 120

Qy 121 POKLAFAECLCRGICIDARTGRETAAALNSVRLQSLIVRRCPSRQDSGLPPTGAFAHFT 180  
 Db 121 pklafeaclcrgicidartgretaaalnsvrlqslivrrcpsrdsqpltpgafahft 180

Qy 181 EPHVPGCTCVLPRSV 197  
 Db 181 ephvpgctcvlprsv 197

CC differentiation or mobilization of immune cells, disorders of hematopoietic cells (e.g. ataxia, human immunodeficiency virus (HIV) infection, anemia, thrombocytopenia), autoimmune disorders (e.g. Grave's disease, systemic lupus erythematosus, ophthalmia), graft versus host disease, inflammatory, hyperproliferative disorders, or infectious diseases. The polypeptides are useful for generating antibodies, which can be used to treat inhibit or prevent diseases or conditions associated with aberrant expression and/or activity of IL-21 or IL-22. The present sequence represents the amino acid sequence of human IL-21. XX Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 22; Length 197;  
Best Local Similarity 100.0%; Pred. No. 4.6e-109; Gaps 0;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MTLLPGILFLFTWLHTCLAHHDPSLRLGRHPSLHGTPHCYSAEELPLGQAPPHLLARGAKWQ 60  
Db 1 mtllpgilflftwlhtclahhdpslrlgrhpslhgtphcyxaeelplgqapphllargakwq 60  
Qy 61 ALPVALYSSLEASHRGHRHERPATTCTCPVLRPEEVLEADTHORSISPSWRYVDTDDRY 120  
Db 61 alpvalyssleashrghrherpattctcpvrlrpeevleadthorsispswryvdtddry 120  
Qy 121 POKLAFAECLCRGICDARTGRTAALNSVRLQSLILVRRICSDRGSLPPPGAFAHF 180  
Db 121 poklafaeclcrsicdartgretaaalnsvrllqslvrricsdrgslpppgafahf 180  
Qy 181 EFPYVPGCTCVLPRSV 197  
Db 181 efpypgctcvlprsv 197  
Qy 181 efpypgctcvlprsv 197

RESULT 8  
AAU29247 AAU29247 standard; Protein; 197 AA.  
XX AC AAU29247;  
XX DT 18-DEC-2001 (first entry)  
XX DE Human PRO polypeptide sequence #224.  
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
OS Homo sapiens.  
XX PN WO/00168848-A2.  
XX PD 20-SEP-2001.  
XX PF 28-FEB-2001; 2001WO-US06520.  
XX PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 03-MAR-2000; 2000US-187202P.  
PR 06-MAR-2000; 2000US-186968P.  
PR 14-MAR-2000; 2000US-189320P.  
PR 14-MAR-2000; 2000US-189328P.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 21-MAR-2000; 2000US-100828P.  
PR 21-MAR-2000; 2000US-191007P.  
PR 21-MAR-2000; 2000US-191048P.  
PR 21-MAR-2000; 2000US-191314P.  
PR 28-MAR-2000; 2000US-192651P.  
PR 29-MAR-2000; 2000US-193032P.  
PR 29-MAR-2000; 2000US-13053P.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 04-APR-2000; 2000US-194449P.

PR 04-APR-2000; 2000US-194647P.  
PR 11-APR-2000; 2000US-195715P.  
PR 11-APR-2000; 2000US-196000P.  
PR 11-APR-2000; 2000US-196187P.  
PR 11-APR-2000; 2000US-196610P.  
PR 18-APR-2000; 2000US-198121P.  
PR 18-APR-2000; 2000US-198385P.  
PR 25-APR-2000; 2000US-199397P.  
PR 25-APR-2000; 2000US-199550P.  
PR 25-APR-2000; 2000US-199544P.  
PR 03-MAY-2000; 2000US-201516P.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 20-MAY-2000; 2000US-201516P.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 05-JUN-2000; 2000US-209832P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 22-AUG-2000; 2000US-0644848.  
PR 24-AUG-2000; 2000WO-US23288.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
XX PA (GETH ) GENENTECH INC.  
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
DR N-PSDB; AAS46148.  
XX PA Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -  
XX PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -  
XX PT Sequences AAU29024 -AAU29328 represent PRO polypeptides of the invention.  
XX PS AAU29024 -AAU29328 represent PRO polypeptides of the invention.  
XX CC The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.  
XX Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 22; Length 197;  
Best Local Similarity 100.0%; Pred. No. 4.6e-109;  
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MTLLPGILFLTWLHTCLAHHDPSLRLGRHPSLHGTPHCYSAEELPLGQAPPHLLARGAKWQ 60  
Db 1 mtllpgilfltwlhtclahhdpslrlgrhpslhgtphcyxaeelplgqapphllargakwq 60  
Qy 61 ALPVALYSSLEASHRGHRHERPATTCTCPVLRPEEVLEADTHORSISPSWRYVDTDDRY 120  
Db 61 alpvalyssleashrghrherpattctcpvrlrpeevleadthorsispswryvdtddry 120  
Qy 121 POKLAFABCLCRGICDARTGRTAALNSVRLQSLILVRRICSDRGSLPPPGAFAHF 180  
Db 121 poklafabclcrsicdartgretaaalnsvrllqslvrricsdrgslpppgafahf 180







PS Claim 18: Page -; 117pp; English.  
 XX The present invention relates to interleukin (IL)-17 like polypeptides  
 CC and nucleic acids encoding them. IL-17 like protein is useful for  
 CC identifying binding partners, agonists and antagonists which can be used  
 CC for treating one or more diseases or disorders and for cloning IL-17  
 CC like receptors, using an expression cloning strategy. Radiolabelled or  
 CC affinity/activity-tagged IL-17 proteins are useful in binding assays to  
 CC identify a cell type or cell line or tissue that expresses IL-17 like  
 CC receptors. A radiolabelled or tagged IL-17 like protein is useful as an  
 CC affinity ligand to identify and isolate from an expression library the  
 CC subset of cells which express the IL-17 like receptors on their surface.  
 CC IL-17 like protein, agonist and antagonist are useful for treating acute  
 CC and chronic inflammation such as rheumatic diseases, graft versus host  
 CC disease and multiple sclerosis. IL-17 like antagonists are useful for  
 CC treating and preventing inflammatory disease, autoimmune disease,  
 CC allergies, asthma and organ or graft rejection in a patient and also  
 CC for inhibiting T cell proliferation and/or activation, in vivo B cell  
 CC proliferation or immunoglobulin secretion, and for blocking the effects  
 CC of IL-17 in inducing bone destruction. IL-17 like molecule is useful in  
 CC gene therapy and for mapping the location of the IL-17 like gene and  
 CC related genes on chromosomes, as hybridisation probes in diagnostic  
 CC assays. Non-human animals in which the promoter for one or more of IL-17  
 CC like protein is either activated or inactivated are useful for drug  
 CC candidate screening. The present sequence is human IL-17 like  
 CC protein mutant (Leu47Ile).  
 CC Note: The present sequence is not shown in the specification, but is  
 CC derived from the human IL-17 like protein referred to as SEQ ID NO:2  
 (AAE08676), shown in figure 1A.  
 XX

SQ Sequence 227 AA;  
 Query Match 98.9%; Score 1061; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1.1e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLPGLEFLTWLHTCLAHHDPSLRGPHSHGTPHCVYSAEFLPLGGQAPPHILARGAKNGQAL 62  
 Db 33 11pgllfltwlhctiahhhdpslrghphshgtpchcysaeellplggqaphillargakngqal 92  
 Qy 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHRSISSPWRYRYVDTDEDRYQ 122  
 Db 93 pvalvssleashrgrherpsattqcpvlrpeevleadtqrsisspwryrvdtdeqyq 152  
 Qy 123 KIAFAECICRGCIDARGRETAALNSVRLQSLVLRPGRDGSLLPTGAFATTEF 182  
 Db 153 kiafaecicrgcidartgretaalnsvrlqslvlrpgrdgsllptgafattef 212  
 Qy 183 IHPVGCGTCVPLRSV 197  
 Db 213 ihpvgctcvplrsv 227

RESULT 14  
 AA08682  
 ID AAE08682 standard; Protein; 227 AA.  
 XX  
 AC AAE08682;  
 XX  
 DT 15 - NOV - 2001 (first entry)

XX Human interleukin (IL)-17 like protein mutant (Leu47Met).  
 DE Human interleukin (IL)-17 like protein mutant (Leu47Met).  
 XX Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;  
 KW multiple sclerosis; graft versus host disease; inflammatory disease;  
 KW asthma; autoimmune disease; allergy; graft rejection; bone destruction;  
 KW drug screening; antiinflammatory; immunosuppressive; antiasthmatics;  
 KW neuroprotective; antirheumatic; antiallergic; mutant; mutein.  
 XX Homo sapiens.  
 OS Synthetic.

FH Key 47 Location/Qualifiers  
 FT Misc-difference /note= "Wild-type Leu substituted with Met"  
 XX  
 FT WO200159120-A2.  
 PN XX  
 PD 16-AUG-2001.  
 PF 07-FEB-2001; 2001WO-US03916.  
 XX  
 PR 08-FEB-2000; 2000US-0180864.  
 PR 27-NOV-2000; 2000US-0722920.  
 XX  
 PA (ANGE-) AMGEN INC.  
 XX  
 PI Jing S, Bass MB;  
 XX  
 DR 2001-529841/58.  
 XX  
 PT Novel interleukin-17 like polypeptides and nucleic acid molecules  
 PT encoding them useful for diagnosis, prevention and treatment of  
 PT inflammatory, autoimmune disease, allergies, asthma and organ or graft  
 PT rejection.  
 XX  
 PA Claim 18; Page -; 117pp; English.  
 XX  
 CC The present invention relates to interleukin (IL)-17 like polypeptides  
 CC and nucleic acids encoding them. IL-17 like protein is useful for  
 CC identifying binding partners, agonists and antagonists which can be used  
 CC for treating one or more diseases or disorders and for cloning IL-17  
 CC like receptors using an expression cloning strategy. Radiolabelled or  
 CC affinity/activity-tagged IL-17 proteins are useful in binding assays to  
 CC identify a cell type or cell line or tissue that express IL-17 like  
 CC receptors. A radiolabelled or tagged IL-17 like protein is useful as an  
 CC affinity ligand to identify and isolate from an expression library the  
 CC subset of cells which express the IL-17 like receptors on their surface.  
 CC IL-17 like protein, agonist and antagonist are useful for treating acute  
 CC and chronic inflammation such as rheumatic diseases, graft versus host  
 CC disease and multiple sclerosis. IL-17 like antagonists are useful for  
 CC treating and preventing inflammatory disease, autoimmune disease,  
 CC allergies, asthma and organ or graft rejection in a patient and also  
 CC for inhibiting T cell proliferation and/or activation, in vivo B cell  
 CC proliferation or immunoglobulin secretion, and for blocking the effects  
 CC of IL-17 in inducing bone destruction. IL-17 like molecule is useful in  
 CC gene therapy and for mapping the location of the IL-17 like gene and  
 CC related genes on chromosomes, as hybridisation probes in diagnostic  
 CC assays. Non-human animals in which the promoter for one or more of IL-17  
 CC like protein is either activated or inactivated are useful for drug  
 CC candidate screening. The present sequence is human IL-17 like  
 CC protein mutant (Leu47Met).  
 CC Note: The present sequence is not shown in the specification, but is  
 CC derived from the human IL-17 like protein referred to as SEQ ID NO:2  
 (AAE08676), shown in figure 1A.  
 XX  
 SQ Sequence 227 AA;  
 Query Match 98.9%; Score 1061; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1.1e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 PT  
 Qy 3 LLPGLEFLTWLHTCLAHHDPSLRGPHSHGTPHCVYSAEFLPLGGQAPPHILARGAKNGQAL 62  
 Db 33 11pgllfltwlhctiahhhdpslrghphshgtpchcysaeellplggqaphillargakngqal 92  
 Qy 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHRSISSPWRYRYVDTDEDRYQ 122  
 Db 93 pvalvssleashrgrherpsattqcpvlrpeevleadtqrsisspwryrvdtdeqyq 152  
 Qy 123 KIAFAECICRGCIDARGRETAALNSVRLQSLVLRPGRDGSLLPTGAFATTEF 182  
 Db 153 kiafaecicrgcidartgretaalnsvrlqslvlrpgrdgsllptgafattef 212  
 Qy 183 IHPVGCGTCVPLRSV 197  
 Db 213 ihpvgctcvplrsv 227

QY 183 IHVPVGCTCIVLPRSV 197  
 DB 213 ihvpvgctcivlprsv 227

RESULT 15  
 ID AAE08681 standard; Protein; 227 AA;  
 XX  
 AC AAE08681;  
 XX 15-NOV-2001 (first entry)  
 XX Human interleukin (IL)-17 like protein mutant (Leu47Val).  
 KW Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;  
 KW multiple sclerosis; graft versus host disease; inflammatory disease;  
 KW asthma; autoimmune disease; allergy; graft rejection; bone destruction;  
 KW drug screening; antiinflammatory; immunosuppressive; antiasthmatic;  
 KW neuroprotective; antirheumatic; antiallergic; mutant; mutein.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 PH Location/Qualifiers  
 FT Misc-difference 47  
 /note= "Wild-type Leu substituted with Val"  
 FT  
 PN W0200159120-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 07-FEB-2001; 2001WO-US03916.  
 XX  
 PR 08-FEB-2000; 2000US-0180864.  
 PR 27-NOV-2000; 2000US-0722920.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Jing S, Bass MB;  
 XX  
 DR 2001-529841/58.

XX Novel interleukin-17 like polypeptides and nucleic acid molecules  
 PT encoding them useful for diagnosis, prevention and treatment of  
 PR inflammatory, autoimmune disease, allergies, asthma and organ or graft  
 PR rejection -  
 XX  
 PS Claim 18; Page -; 117PP; English.  
 XX  
 CC The present invention relates to interleukin (IL)-17 like polypeptides  
 CC and nucleic acids encoding them. IL-17 like protein is useful for  
 CC identifying binding partners, agonists and antagonists which can be used  
 CC for treating one or more diseases or disorders and for cloning IL-17  
 CC like receptors, using an expression cloning strategy. Radiolabelled or  
 CC affinity/activity-tagged IL-17 proteins are useful in binding assays to  
 CC identify a cell type or cell line or tissue that express IL-17 like  
 CC receptors. A radiolabelled or tagged IL-17 like protein is useful as an  
 CC affinity ligand to identify and isolate from an expression library the  
 CC subset of cells which express the IL-17 like receptors on their surface.  
 CC IL-17 like protein, agonist and antagonist are useful for treating acute  
 CC and chronic inflammation such as rheumatic diseases, graft versus host  
 CC disease and multiple sclerosis. IL-17 like antagonists are useful for  
 CC treating and preventing inflammatory disease, autoimmune disease,  
 CC allergies, asthma and organ or graft rejection in a patient and also  
 CC for inhibiting T cell proliferation and/or activation, in vivo B cell  
 CC proliferation or immunoglobulin secretion, and for blocking the effects  
 CC of IL-17 in inducing bone destruction. IL-17 like molecule is useful in  
 CC gene therapy and for mapping the location of the IL-17 like gene and  
 CC related genes on chromosomes, as hybridisation probes in diagnostic  
 CC assays. Non human animals in which the promoter for one or more of IL-17  
 CC like protein is either activated or inactivated are useful for drug  
 CC candidate screening. The present sequence is human IL-17 like

protein mutant (Leu47Val).  
 Note: The present sequence is not shown in the specification, but is  
 derived from the human IL-17 like protein referred to as SEQ ID NO:2  
 (AAE08676), shown in figure 1A.

RESULT 15  
 ID AAE08681 standard; Protein; 227 AA;  
 XX  
 AC AAE08681;  
 XX 15-NOV-2001 (first entry)  
 XX Human interleukin (IL)-17 like protein mutant (Leu47Val).  
 KW Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;  
 KW multiple sclerosis; graft versus host disease; inflammatory disease;  
 KW asthma; autoimmune disease; allergy; graft rejection; bone destruction;  
 KW drug screening; antiinflammatory; immunosuppressive; antiasthmatic;  
 KW neuroprotective; antirheumatic; antiallergic; mutant; mutein.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 PH Location/Qualifiers  
 FT Misc-difference 47  
 /note= "Wild-type Leu substituted with Val"  
 FT  
 PN W0200159120-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 07-FEB-2001; 2001WO-US03916.  
 XX  
 PR 08-FEB-2000; 2000US-0180864.  
 PR 27-NOV-2000; 2000US-0722920.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Jing S, Bass MB;  
 XX  
 DR 2001-529841/58.

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

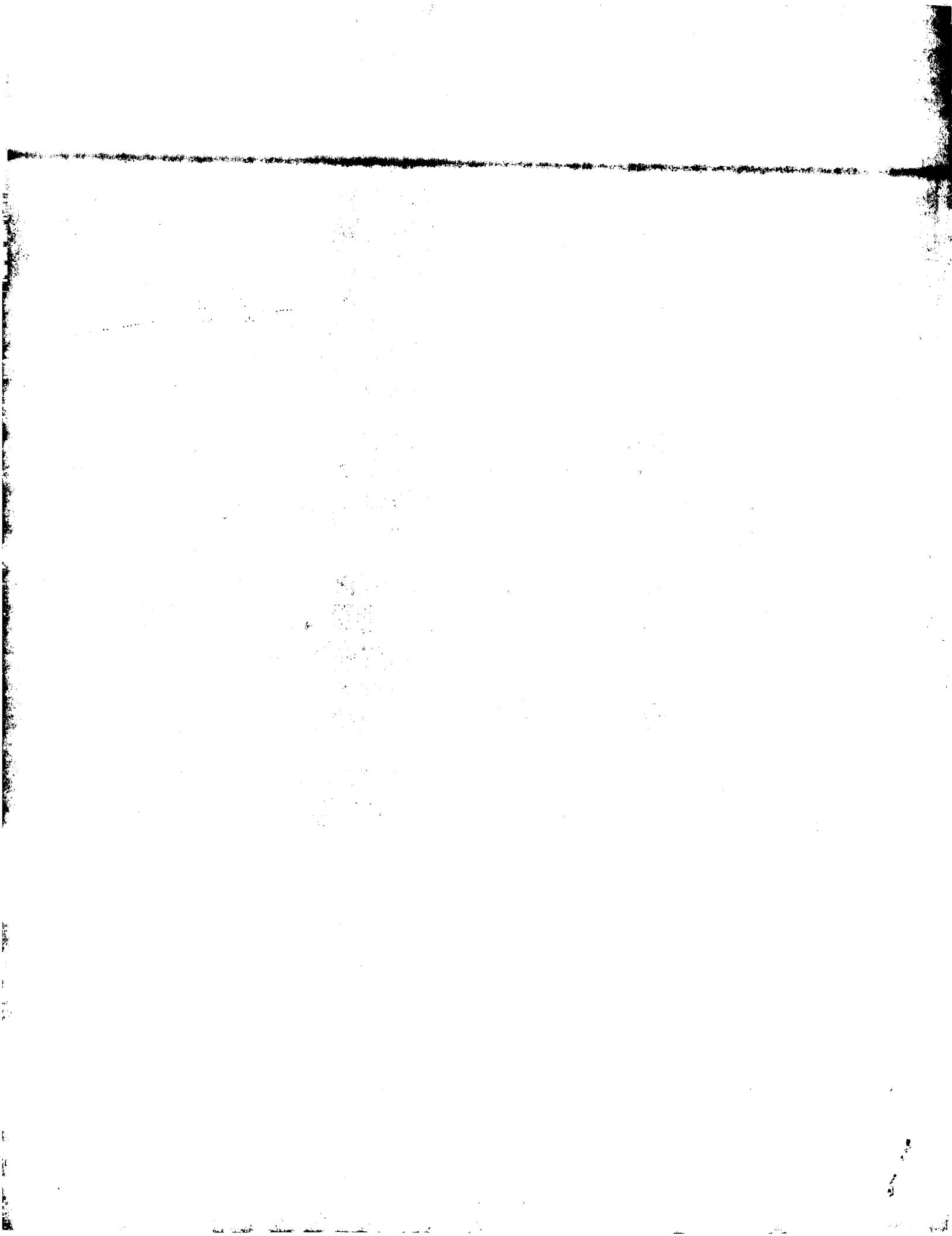
QY 3 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 62  
 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

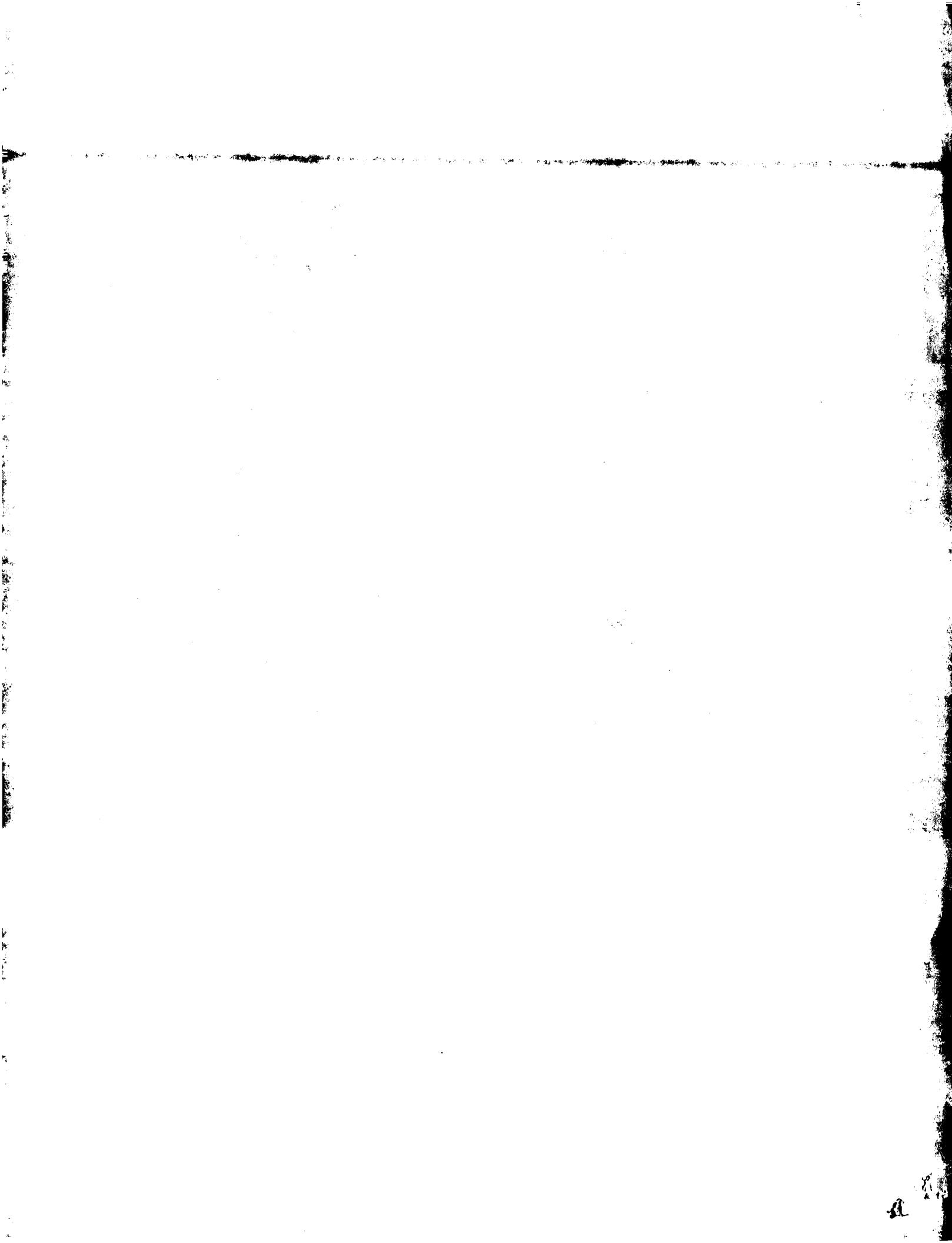
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 Db 33 LIPGLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPQGQAPHLARGAKNGOAL 92  
 QY 63 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 122  
 Db 93 PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPVWRYVDTDDEDRYPO 152  
 QY 123 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 182  
 Db 153 KIAFAECLURGCIDARTGRETAAALNSVRLQSLVLLRRCPSRDGSGLPTPCAFAFHTEF 212

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1 5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 L

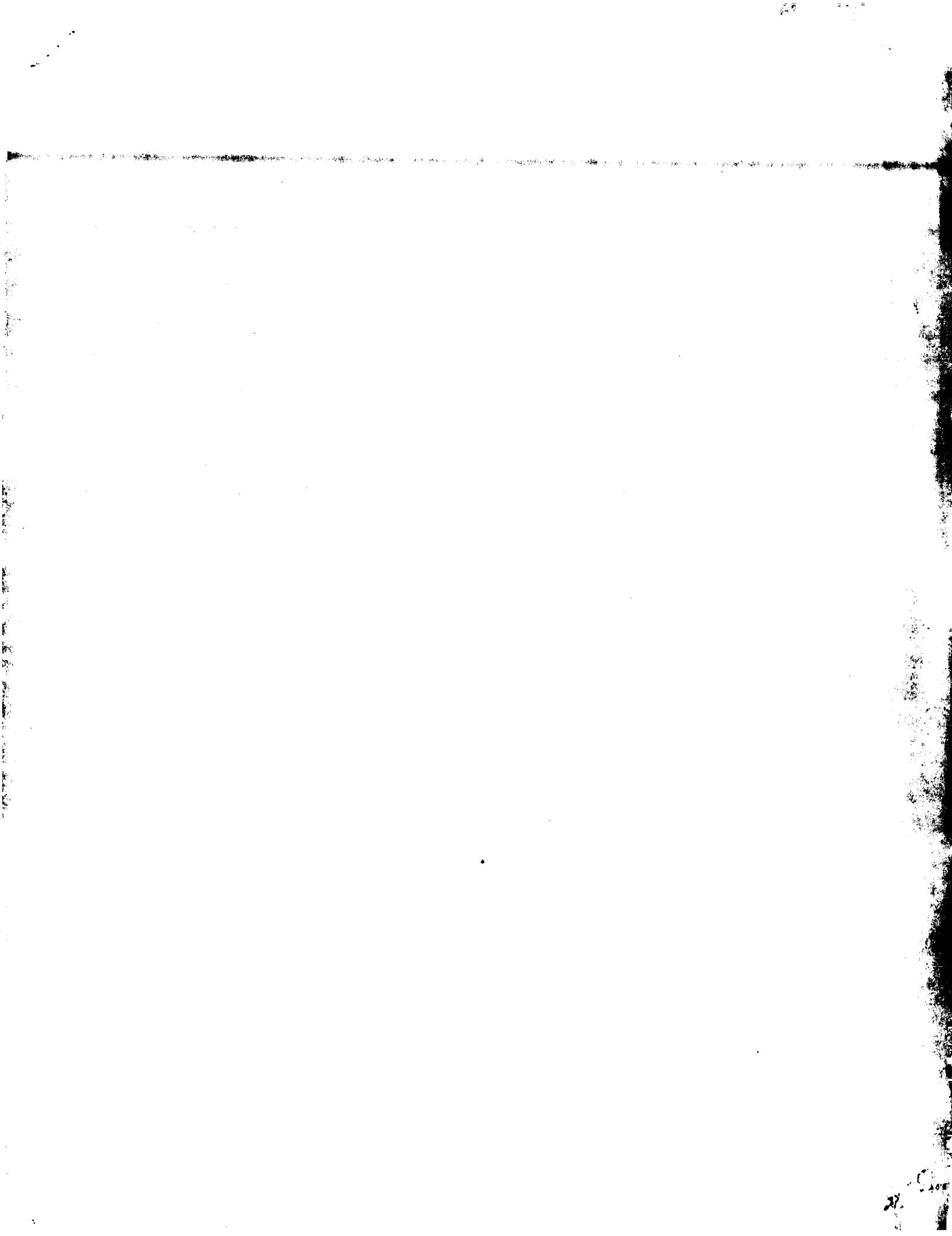


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Best Local Similarity:	100.0%;	Pred. No.:	4.6e-109;		DR	NP-PSDB; AAZ29728.
Matches:	197;	Conservative:	0;	Mismatches:	0;	New polypeptides designated PRO1031 and PRO1122 used to treat a degenerative cartilaginous disorder
Qy	1	MILLPGLEFLFLWLTCLAHHDPSLGRPHPSHGTPHCSAELPLGQAPPILLARGAKWGO	60	PT	XX	
Db	1	mtllpglfiflwltclahhdpslgrphpshgtphcysaelpgqappillargakwgq	60	PT	XX	
Qy	61	ALPVALVSSLEAAASHRGRHERRPSATTQCPVLRPEEVLEADTHQRSTSPWRYRVDTDEDRY	120	PT	XX	
Db	61	alpvalvssleaaashrgrherrpsattqcpvlpreevleadtqrsispwryrvdtdeiry	120	PT	XX	
Qy	121	PQKLAFAECLRGCCDARTGRETAAALNSVRLQSLVLRRPCSRDGSLPTPGAFAFHT	180	PT	XX	
Db	121	pqklafaeclrgccdartgretaaalnsvrlqlsllvrrpcsrdsqsgtpgafafht	180	PT	XX	
Qy	181	EPIHYPVGCTVLPYRV 197	197	PS	XX	
Db	181	efihypvgctvlpysv 197	197	PS	XX	
Qy	181	EPIHYPVGCTVLPYRV 197	197	PS	XX	
Db	181	efihypvgctvlpysv 197	197	PS	XX	
RESULT	5				Query Match	100.0%;
AY44460					Best Local Similarity	100.0%;
ID	AY44460	standard;	Protein;	197 AA.	Matches	197;
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AC	AY44460;				Mismatches	0;
XX					Indels	0;
DT	27-MAR-2000	(first entry)			Gaps	0;
DE	Human Interleukin 17C, PRO1122 polypeptide.					
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Interleukin; IL-17C; PRO1122 polypeptide; clone DNA62377-1381-1; UNQ561;						
cytokine IL-17; cytotoxic T-lymphocyte-associated antigen 8; CTLA-8;						
hybridisation probe; antagonist; degenerative cartilaginous disorder;						
agonist; diagnose; therapy.						
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CS	Homo sapiens.					
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Key	Location/Qualifiers					
Peptide	1.18					
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Protein	/label= Signal_peptide					
FT	/label= Mature_IL-17C-polypeptide					
FT	/note= "Used to treat degenerative cartilaginous					
FT	disorder"					
FT	Misc-difference 109					
FT	Misc-difference 129					
FT	/note= "Conserved Trp residue"					
FT	Misc-difference 134					
FT	/note= "Conserved Cys residue"					
FT	Misc-difference 163					
FT	/note= "Conserved Cys residue"					
FT	Misc-difference 189					
FT	/note= "Conserved Cys residue"					
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PR	23-DEC-1998;					
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PA	(GETH ) GENENTECH INC.					
XX						
PI	Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI;					
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FT	25-NOV-1999.					
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PI	Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI;					
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FT Domain /note= "conserved domain I"  
 FT FT 129..134.  
 FT Domain /note= "conserved domain II"  
 FT FT 156..162.  
 FT Domain /note= "conserved domain III"  
 FT FT 185..192.  
 FT FT /note= "conserved domain IV"  
 XX PN WO9961617-A1.  
 XX XX  
 PD 02-DEC-1999.  
 XX XX  
 PF 27-MAY-1999; 99WO-US1644.  
 XX XX  
 PR 29-MAY-1998; 98US-0087340.  
 PR 10-SEP-1998; 98US-009805.  
 PR 30-APR-1999; 99US-0131965.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Ruben SM, Ebner R;  
 XX DR WPI; 2000-072622/06.  
 DR N-FSDB; AAZ36836.  
 XX  
 PS Claim 26; Fig 6A-B; 170pp; English.  
 XX  
 CC The present sequence represents a human interleukin-21 (IL-21) protein. The specification also describes IL-22 polynucleotides and polypeptides. The IL-21 polynucleotide was isolated from a cDNA library of apoptotic T-cells. IL-21 and IL-22 may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells, treating or detecting deficiencies or disorders of haematopoietic cells, to modulate haemostatic or thrombolytic activity, in treating or detecting autoimmune disorders, treating asthma (particularly allergic asthma) or other respiratory problems, to treat and/or prevent organ rejection or graft-versus-host disease (GVHD), to modulate inflammation, to treat or detect hyperproliferative disorders, to treat or detect infectious agents, to differentiate, proliferate and attract cells, leading to the regeneration of tissues, IL-21 and IL-22 may also increase or decrease the differentiation or proliferation of embryonic stem cells and haematopoietic lineage, may be used to modulate mammalian characteristics.  
 XX SQ Sequence 197 AA;  
 XX  
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 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MTLLPQIULFTLWHTCIAHHIDPSLRGPHPHSGTGHGTCYSAEFLPLGQAPPHILLARGAKWGQ 60  
 Db 1 mtllpqliflwhtclahpslghphsgtghphsgtghphsgtphcysaaslpqgphillargakwgq 60  
 Qy 61 ALPVALVSSLEAASHRGRHFRPSATQCPVLRPEEVLLEADTHQRSLSPWWRVDDEDR 120  
 Db 61 alpvalvssleashrgrhfrpsatqcpvlrpeevleadtqrspswprvddedr 120  
 Qy 121 POKLAAECIQLRGCDIARTGRETAAALNSVRLQSLIVLRRPCSRDGSGLPTGAFAFHT 180  
 Db 121 pqklaaeciqlrgcdiartgretaaalnsvrlqslivlrrpcsrdfsglpptgafafht 180  
 Qy 181 EFIHVPGCTCVLPRSV 197  
 Db 181 efihvpgctcvlprsv 197

RESULT 7  
 ID AAG66121  
 ID AAG66121 standard; Protein; 197 AA.  
 XX  
 AC AAG66121;  
 XX  
 DT 13-MAR-2002 (first entry)  
 XX  
 DE Human Interleukin (IL)-21 amino acid sequence.  
 XX KW Interleukin; IL-21; IL-22; immunosuppressive; cytostatic; thrombolytic;  
 KW antiinflammatory; antibacterial; gene therapy; human.  
 XX OS Homo sapiens.  
 XX  
 Key FH Location/Qualifiers  
 Peptide FT 1..18  
 Protein FT 19..197  
 Protein FT /note= "mature protein"  
 Domain FT 34..40  
 Domain FT /note= "conserved domain V"  
 Domain FT 63..68  
 Domain FT /note= "conserved domain VI"  
 Domain FT 104..109  
 Domain FT /note= "conserved domain VII"  
 Domain FT 113..121  
 Domain FT /note= "conserved domain I"  
 Domain FT 129..134  
 Domain FT /note= "conserved domain II"  
 Domain FT 156..162  
 Domain FT /note= "conserved domain III"  
 Domain FT 185..192  
 Domain FT /note= "conserved domain IV"  
 PN US2001023070-A1.  
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 PD 20-SEP-2001.  
 XX  
 PR 08-DEC-2000; 2000US-0731816.  
 XX  
 PR 29-MAY-1998; 98US-087340P.  
 PR 30-APR-1999; 99US-111965P.  
 PR 27-DEC-1999; 99US-169837P.  
 PR 27-MAY-1999; 99US-0320713.  
 PR 27-MAY-1999; 99WO-US11644.  
 PA (EBNER/) EBNER R.  
 PA (RUBE/) RUBEN S M.  
 XX  
 PI Ebner R, Ruben SM;  
 XX  
 DR WPI; 2001-638470/73.  
 DR N-PSDB; AA167878.  
 XX  
 PT New interleukin-21 and interleukin-22 polynucleotides and polypeptides,  
 PT useful for treating, preventing or diagnosing e.g. disorders of  
 PT hematopoietic cells, autoimmune disorders, or hyperproliferative  
 PT diseases.  
 XX  
 Claim 26; Fig 6A-B; 87pp; English.  
 XX  
 CC The invention relates to novel human proteins designated interleukin  
 CC (IL)-21 and IL-22. The IL-21 and IL-22 polynucleotides can be used in  
 CC linkage analysis as a marker for those specific chromosome, in chromosome  
 CC mapping, to control gene expression through triple helix formation or  
 CC antisense DNA or RNA, in gene therapy, in identifying individuals from  
 CC minute biological samples, as an alternative to restriction fragment  
 CC length polymorphism (RFLP) analysis, as polymorphic markers for forensic  
 CC purposes, as molecular weight markers, or as diagnostic probes. IL-21 and  
 CC IL-22 polypeptides can be used to treat, prevent or diagnose diseases of  
 CC the immune system by activating or inhibiting the proliferation,



Result No.	Score	Query Match	Length	DB	ID	Description
1	1073	100.0	197	4	Q9P0m4	Q9P0m4 homo sapien
2	1065	99.3	197	4	Q9IC75	Q9hc75 homo sapien
3	173	16.1	109	4	Q96p18	Q96p18 homo sapien
4	173	16.1	163	4	Q96pD4	Q96pD4 homo sapien
5	169.5	15.8	180	11	Q99MY3	Q99my3 mus musculus
6	168.5	15.7	180	11	Q9QXT6	Q9qxt6 mus musculus
7	165.5	15.4	177	4	Q9I293	Q9h293 homo sapien
8	160.5	15.0	215	11	Q9CT14	Q9ct14 mus musculus
9	157.5	14.7	151	12	Q9E033	Q9hc75 saimiriine
10	157.5	14.7	178	11	Q9E016	Q9eqi16 mesocricetus
11	157	14.6	141	6	Q9I156	Q9i156 bos taurus
12	154.5	14.4	180	4	Q9DHF5	Q9uhf5 homo sapien
13	136	12.7	78	4	Q9NE6	Q9ne6 homo sapien
14	129.5	12.1	111	11	Q9EQ17	Q9eqi7 rattus norvegicus
15	110	10.3	148	5	Q19778	Q19778 caenorhabditis elegans
16	95.5	8.9	93	6	Q9BEH5	Q9beh5 equus caballus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

SEQUENCE FROM N.A.  
 RX MIDDLEINP=20105548; PubMed=10639955;  
 RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,  
 RA Gurney A.L., Wood W.L.;  
 RT "Cloning and Characterization of IL-17B and IL17C, Two New Members of the IL-17 Cytokine Family";  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).  
 RL AF152099; AAF28105.1;  
 DR EMBL: AF152099; BAE0152E18DE7D08 CRC64;  
 SQ SEQUENCE 197 AA; 21765 MW;

SEQUENCE FROM N.A.  
 RX MIDDLEINP=20105548; PubMed=10639955;  
 RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,  
 RA Gurney A.L., Wood W.L.;  
 RT "Cloning and Characterization of IL-17B and IL17C, Two New Members of the IL-17 Cytokine Family";  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).  
 RL AF152099; AAF28105.1;  
 DR EMBL: AF152099; BAE0152E18DE7D08 CRC64;

Query Match 100.0%; Score 1073; DB 4; Length 197;  
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 QY 1 MTLLPGFLFLWLUHTCLAHHDPSLRLGHPSHGTPHCYSAEELPLGQAPPHILARGKKGQ 60  
 DB 1 MTLLPGFLFLWLUHTCLAHHDPSLRLGHPSHGTPHCYSAEELPLGQAPPHILARGKKGQ 60  
 QY 61 ALPVALVSSLEASHGRHERPSATQCPVLRPEEYLEADTHORSTSPWRYRVDTEDRY 120  
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 DB 61 ALPVALVSSLEASHGRHERPSATQCPVLRPEEYLEADTHORSTSPWRYRVDTEDRY 120

QY 121 PQKLAFAECLCRGICIDARTGRETAAALNSVRLLQSLYLRRRPCSRSGSLPTPGAFAFHT 180  
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Qy	181	EFTHVPVGCTCVLPRSV	197	Best Local Similarity 39.0%; Predicted No. 5.7e-10;
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Db				
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ID	Q9HC75			
AC	Q9HC75;			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)		
DE	CYTOKINE CX2 PRECURSOR.			
OS	Homo sapiens (Human).			
RA	Zhang W., He L., Wan T., Yuan Z., Cao X.;			
RT	"Novel human cytokine CX2 with homology to IL-17.";			
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: APL42410; AAC27921.1; -.			
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RA	Zhang W., He L., Wan T., Yuan Z., Cao X.;			
RT	"Novel human cytokine CX2 with homology to IL-17.";			
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: APL42410; AAC27921.1; -.			
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Best Local Similarity 99.5%; Predicted No. 1.3e-99;				
Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	1	MTRLPGLIPLFLWLTCLAHHDPSLRGPHPHSHTPHCYSAEELPLGQAPPHLARGAKWQ	60	Best Local Similarity 39.0%; Predicted No. 9.9e-10;
Db	1	MTRLPGLIPLFLWLTCLAHHDPSLRGPHPHSHTPHCYSAEELPLGQAPPHLARGAKWQ	60	Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;
Qy	61	ALPVALYSSLEASHRGRHERPSATTQCPVLRPEEVLEADTHQRSTSPWLRVTDDEDRY	120	
Db	61	ALPVALYSSLEASHRGRHERPSATTQCPVLRPEEVLEADTHQRSTSPWLRVTDDEDRY	120	
Qy	121	POKLAFAECLRCRCCIDARTGRETAAALNSVRLQLSLVLRREPCSRDGSGLPTPGAFAH	180	Best Local Similarity 39.0%; Predicted No. 9.9e-10;
Db	121	POKLAFAECLRCRCCIDARTGRETAAALNSVRLQLSLVLRREPCSRDGSGLPTPGAFAH	180	Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;
Qy	181	EFTHVPVGCTCVLPRSV	197	
Db	181	EFTHVPVGCTCVLPRSV	197	
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AC	Q9EP18;			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
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DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
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OS	Homo sapiens (Human).			
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID	9606;			
RP	SEQUENCE FROM N.A.			
RA	Kawaguchi M., Onuchic L.F., Li X.-D., Essayer D.M., Schroeder J., Xiao H.-Q., Liu M.C., Krishnasamy G., Germino G., Huang S.-K.;			
RT	"Identification of a Novel Cytokine, ML-1, and Its Expression in Subjects with Asthma.";			
RT	J. Immunol. 167:4430-4435 (2001).			
DR	EMBL: AF332289; AAL14427.1; -.			
SQ	SEQUENCE 109 AA; 12327 MW; 52C5B34C36DC30BB CRC64;			
Query Match	16.1%	Score: 173; DB 4; Length: 109;		
Query Match	15.8%	Score: 169.5; DB 11; Length: 180;		

Best Local Similarity 27.0%; Pred. No 2.2e-09;	Matches 53; Conservative 28; Mismatches 82; Indels 33; Gaps 6;	Qy 7 LLFLTLWHTCLA-HHDPSSLRGRPHSHGTGPHYSAAEELPLGAPPHILLARGAKWQALPVA 65	Qy 177 AFHTEF1HVPVNGCTV 192
Db 7 LLFLTLAISFLAPSHRNTKRGKGKPS-----HOVPLD 48	Db 164 RQRVVMETIAVGCTC 179	Db 7 LLFLTLAISFLAPSHRNTKRGKGKPS-----HOVPLD 48	Db 164 RQRVVMETIAVGCTC 179
Qy 66 LVSSLEASHGRHERPSATQCPVLRPEYEAD-----THQRSTSPWRVRYDTD 116	RESULT 7	Qy 66 LVSSLEASHGRHERPSATQCPVLRPEYEAD-----THQRSTSPWRVRYDTD 116	RESULT 7
Db 49 LVSRVKPYARMEYEYERLGENVAAQLRNSSEPAKKCEVNQLWLWSNKRSLSPWGVSINHD 108	Q9H293 PRELIMINARY; ID Q9H293 AC DT 01-MAR-2001 (TREMBLrel. 16, Created)	Db 49 LVSRVKPYARMEYEYERLGENVAAQLRNSSEPAKKCEVNQLWLWSNKRSLSPWGVSINHD 108	Q9H293 PRELIMINARY; ID Q9H293 AC DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
Qy 117 EDRYPTQKLAFAECLCRGCIADRTGRTAAALNSVRLQLSLLVLRREPCSDRGSLPTPGAF 176	DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)	Qy 117 EDRYPTQKLAFAECLCRGCIADRTGRTAAALNSVRLQLSLLVLRREPCSDRGSLPTPGAF 176	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
Db 109 PSRIPADLPEARCLCLGCVNFTMQEDRSMSVSPVF-SQPVFRRLCPQP---PRPGPC 163	DE INTERLEUKIN 17E.	Db 109 PSRIPADLPEARCLCLGCVNFTMQEDRSMSVSPVF-SQPVFRRLCPQP---PRPGPC 163	DE INTERLEUKIN 17E.
Qy 177 AFHTEF1HVPVNGCTV 192	GN Homo sapiens (Human).	Qy 177 AFHTEF1HVPVNGCTV 192	GN Homo sapiens (Human).
Db 164 RQRVVMETIAVGCTC 179	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. [1]	Db 164 RQRVVMETIAVGCTC 179	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. [1]
RESULT 6	SEQUENCE FROM N.A.	RESULT 6	SEQUENCE FROM N.A.
Q9QXT6 ID Q9QXT6 PRELIMINARY; AC Q9QXT6; PRT; 180 AA.	SEQUENCE FROM N.A.	Q9QXT6 ID Q9QXT6 PRELIMINARY; AC Q9QXT6; PRT; 180 AA.	SEQUENCE FROM N.A.
AC Q9QXT6; PRT; 180 AA.	Best Local Similarity 29.7%; Pred. No. 5.5e-09; Matches 52; Conservative 16; Mismatches 70; Indels 37; Gaps 7;	AC Q9QXT6; PRT; 180 AA.	Best Local Similarity 29.7%; Pred. No. 5.5e-09; Matches 52; Conservative 16; Mismatches 70; Indels 37; Gaps 7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)	Qy 27 HPHSQGTPHCYS-----AEEPLQGQPHILLARGAKWQALPVALVSSLEASHRRRHER 81	DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	Qy 27 HPHSQGTPHCYS-----AEEPLQGQPHILLARGAKWQALPVALVSSLEASHRRRHER 81
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	Db 31 HTYSHWPSCCPBKQDGTSEEL-----LRY-STVP---UPPLEPARPNRHPE 73	DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)	Db 31 HTYSHWPSCCPBKQDGTSEEL-----LRY-STVP---UPPLEPARPNRHPE 73
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)	Qy 82 PSATTCOPVLRPEEVLEADTHRSWYRVDTDDPQLKAFNECLCRGCIADRTGR 141	DE CYTOKINE-LIKE PROTEIN ZCYT07 (NEURONAL INTERLEUKIN-17 RELATED FACTOR)	Qy 82 PSATTCOPVLRPEEVLEADTHRSWYRVDTDDPQLKAFNECLCRGCIADRTGR 141
DE CYTOKINE-LIKE PROTEIN ZCYT07 (NEURONAL INTERLEUKIN-17 RELATED FACTOR)	Db 74 CRASEDPL-----NSRAISIWSWYEDLDRDNLRLPDLHYHRLCPHCVSLQGTS 122	DE CYTOKINE-LIKE PROTEIN ZCYT07 (NEURONAL INTERLEUKIN-17 RELATED FACTOR)	Db 74 CRASEDPL-----NSRAISIWSWYEDLDRDNLRLPDLHYHRLCPHCVSLQGTS 122
DE CYTOKINE-LIKE PROTEIN ZCYT07 (NEURONAL INTERLEUKIN-17 RELATED FACTOR)	Qy 142 E7AAL-NSVRLQSLVIRRPPCSRDGSGLPTGAFAFHTEFTHVPGCTVYLP 195	DE CYTOKINE-LIKE PROTEIN ZCYT07 (NEURONAL INTERLEUKIN-17 RELATED FACTOR)	Qy 142 E7AAL-NSVRLQSLVIRRPPCSRDGSGLPTGAFAFHTEFTHVPGCTVYLP 195
DE CYTOKINE-LIKE PROTEIN ZCYT07 (NEURONAL INTERLEUKIN-17 RELATED FACTOR)	Db 123 HMDPGRNSELLYHNQTVFVYRRECHGNG--THKGTCLERRLYRVSACVYRPR 174	DE CYTOKINE-LIKE PROTEIN ZCYT07 (NEURONAL INTERLEUKIN-17 RELATED FACTOR)	Db 123 HMDPGRNSELLYHNQTVFVYRRECHGNG--THKGTCLERRLYRVSACVYRPR 174
OS Mus musculus (Mouse).	RESULT 8	OS Mus musculus (Mouse).	RESULT 8
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus. [1]	Q9CT14 PRELIMINARY; ID Q9CT14 AC DT 01-JUN-2001 (TREMBLrel. 17, Created)	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus. [1]	Q9CT14 PRELIMINARY; ID Q9CT14 AC DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
QX NCBI_TAXID=10090; RN [1]	Db 74 CRASEDPL-----NSRAISIWSWYEDLDRDNLRLPDLHYHRLCPHCVSLQGTS 122	QX NCBI_TAXID=10090; RN [1]	Db 74 CRASEDPL-----NSRAISIWSWYEDLDRDNLRLPDLHYHRLCPHCVSLQGTS 122
RP Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	Qy 142 E7AAL-NSVRLQSLVIRRPPCSRDGSGLPTGAFAFHTEFTHVPGCTVYLP 195	RP Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	Qy 142 E7AAL-NSVRLQSLVIRRPPCSRDGSGLPTGAFAFHTEFTHVPGCTVYLP 195
RA Moore E.E., Presnell S., Garrigues U., Guillot A., LeGuerin E., Smith D., Yao L., Whitmore T., Gilbert T., Kuestner R.E.; Martinez T., Hoffman R., O'Hara P.; Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	Db 1110006016RK PROTEIN (FRAGMENT).	RA Moore E.E., Presnell S., Garrigues U., Guillot A., LeGuerin E., Smith D., Yao L., Whitmore T., Gilbert T., Kuestner R.E.; Martinez T., Hoffman R., O'Hara P.; Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	Db 1110006016RK PROTEIN (FRAGMENT).
RA SEQUENCE FROM N.A.	GN IL17B OR 1110006016RK.	RA SEQUENCE FROM N.A.	GN IL17B OR 1110006016RK.
RA SEQUENCE FROM N.A.	OS Mus musculus (Mouse).	RA SEQUENCE FROM N.A.	OS Mus musculus (Mouse).
RA Moore E.E., Presnell S., Garrigues U., Guillot A., LeGuerin E., Smith D., Yao L., Whitmore T., Gilbert T., Kuestner R.E.; Martinez T., Hoffman R., O'Hara P.; Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	Db 123 HMDPGRNSELLYHNQTVFVYRRECHGNG--THKGTCLERRLYRVSACVYRPR 174	RA Moore E.E., Presnell S., Garrigues U., Guillot A., LeGuerin E., Smith D., Yao L., Whitmore T., Gilbert T., Kuestner R.E.; Martinez T., Hoffman R., O'Hara P.; Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	Db 123 HMDPGRNSELLYHNQTVFVYRRECHGNG--THKGTCLERRLYRVSACVYRPR 174
RA SEQUENCE FROM N.A.	RP STRAIN=C57BL/6J; TISSUE=EMBRYO; MEDLINE=21085660; PubMed=11217851;	RA SEQUENCE FROM N.A.	RP STRAIN=C57BL/6J; TISSUE=EMBRYO; MEDLINE=21085660; PubMed=11217851;
RA SEQUENCE FROM N.A.	RA Kawai J., Shinagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y., Hara A., Fukunishi Y., Konno H., Adachi J., Kuroda S., Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saico R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King S., Kochiwa H., Kueh P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackerbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,	RA SEQUENCE FROM N.A.	RA Kawai J., Shinagawa A., Shibusawa K., Yoshino M., Itoh M., Ishii Y., Hara A., Fukunishi Y., Konno H., Adachi J., Kuroda S., Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Yamamoto I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saico R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King S., Kochiwa H., Kueh P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackerbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,



Best Local Similarity 40.0% ; Pred. No. 3.1e-08 ; Matches 38 ; Conservative 13 ; Mismatches 34 ; Indels 10 ; Gaps 3 ;		SQ SEQUENCE 180 AA; 20437 MW; F1B0BC146D0B14A CRC64;	
QY 100 DTHRSISWPWYKVDTDEDPOKLAFAECLRGCIDARTGRETAAALNSVRLQLQSLVLR 159		Query Match 14.4% ; Score 154.5 ; DB 4 ; Best Local Similarity 28.7% ; Pred. No. 7.3e-08 ; Matches 45 ; Conservative 25 ; Mismatches 70 ; Indels 17 ; Gaps	
DB 51 DVIKRSRSPWTHLRNPERVSYIWIWAKCSHGSCLNAE-GRVYDHMNSVTIQQEILVLR 109			
QY 160 RPPCSRDSGLPDPGAFAHTTEFHYPVGCCTVLP 194		QY 45 GQAPPHLIARGAKWQALPVAVSSHLRHERPSATTQCPVLRPEEYELAD--- 100	
DB 110 ----RESQHCP---HSFRLKMLVAVGCTCVTP 135		DB 31 GQRRGPAPGP---HOPLDLVSRMKEYARBEYERNIEENVAQLRNSSEIAQRKEVN 87	
RESULT 12		QY 101 ----THQRSISWPWYKVDTDEDPOKLAFAECLRGCIDARTGRETAAALNSVRLQLQSLI 155	
Q90HFS5 PRELIMINARY; PRT; 180 AA.		DB 88 LQLWMSNRSLSWPWGSINHDPSRIPVDPLEPARCLCIGCVNPFTMQDRSAYSVPVE-SQ 146	
AC Q9HFS5; (TREMBLrel. 13, Created)		QY 156 LVLRPDRPSRDSGLPDPGAFAHTTEFHYPVGCCTV 192	
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)		DB 147 VPVYRRLCRLPPP----PTGPCCRORAVMETIAVGCTC 179	
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE CYTOKINE-LIKE PROTEIN ZCYTO7 (INTERLEUKIN 17B)			
DE (NEURONAL INTERLEUKIN-17 RELATED FACTOR) (INTERLEUKIN-17B)			
GN ZCYTO7 OR IL20 OR IL17B.			
OS Homo sapiens (Human).		RESULT 13	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Q9NUE6 PRELIMINARY; PRT; 78 AA.	
OC NCBITaxonID=9606;		AC Q9NUE6; (TREMBLrel. 15, Created)	
OX (1)		DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
RP SEQUENCE FROM N.A.		DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
RA Presnelli S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J., Martinez T., Hoffinan R., O'Hara P., Submitted (Sep-1999) to the EMBL/GenBank/DBJ databases.		DE D0108C2_3 (PUTATIVE NOVEL PROTEIN SIMILAR TO IL17 (INTERLEUKIN 17 (CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED SERINE ESTERASE 8)) (CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED ANTIGEN 8, CTLA8)) (FRAGMENT).	
RN (2)		DE D0108C2_3.	
RP SEQUENCE FROM N.A. MEDLINE-2031718; PubMed=10749887;		OS Homo sapiens (Human).	
RA Barber M.C., Ulrich S.J., Zhang J., Connolly K., Grzegorzewski K.J., Ruben S.M., Knyazev I., Hodde V., Fisher C.B., Olsen H., Gurney A.L., Wood W.I., Stinson J., Heldens S., Foster J., Dowd P., Carroll J.A., Cho Y.H., Kao V., Wilkinson K.A., Eber R.; RR "Cloning and Characterization of IL-17B and IL17C, Two New Members of the IL-17 Cytokine Family"; RR "A novel cytokine receptor-ligand pair. Identification, molecular characterization, and in vivo immunomodulatory activity"; RR Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
RN (3)		RN (1)	
RP SEQUENCE FROM N.A. MEDLINE-20105548; PubMed=10639155;		RP SEQUENCE FROM N.A.	
RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P., Gurney A.L., Wood W.I.; RR "Cloning and Characterization of IL-17B and IL17C, Two New Members of the IL-17 Cytokine Family"; RR "Identification of a novel IL-17 related factor. Demonstration of neuronal expression and evaluation as a candidate for the chromosome 5q-linked form of Charcot-Marie-Tooth disease"; RR Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (4)		RA (1)	
RP SEQUENCE FROM N.A. Moore E.E., Presnelli S., Garrigues U., Guilbot A., LeGuern E., Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.; RR "Novel cytokine homology with interleukin-17"; RR Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (5)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., Nickerson D., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (6)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (7)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (8)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (9)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (10)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (11)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (12)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (13)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (14)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (15)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (16)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (17)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (18)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (19)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (20)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (21)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (22)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (23)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (24)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (25)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (26)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (27)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (28)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (29)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (30)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (31)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (32)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (33)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (34)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (35)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (36)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (37)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (38)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (39)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (40)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (41)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (42)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (43)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (44)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (45)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (46)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (47)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (48)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (49)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (50)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (51)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (52)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (53)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (54)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (55)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (56)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (57)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (58)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (59)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (60)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (61)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (62)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (63)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (64)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (65)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (66)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (67)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (68)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (69)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (70)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (71)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (72)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (73)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (74)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (75)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (76)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (77)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (78)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (79)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (80)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (81)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (82)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (83)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (84)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (85)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (86)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (87)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (88)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (89)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (90)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (91)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (92)		RA (1)	
RP SEQUENCE FROM N.A. Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poelj C.L., Yi Q., RR Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		RA (1)	
RN (93)		RA (1)	

RT "Identification of a novel IL-17 related factor: Demonstration of neuronal expression and evaluation as a candidate for the chromosome 5q-linked form of Charcot-Marie-Tooth disease.";  
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBBJ databases.  
 DR EMBL: AF218724; AAG44133.1;  
 FT NON\_TER 1  
 FT NON\_TER 111 111  
 SQ 111 AA: 12628 MW: D1598392981BA867 CRC64;

Query Match 12.1%; Score 129.5; DB 11; Length 11;  
 Best Local Similarity 37.8%; Pred. No. 1.4e-05;  
 Matches 28; Conservative 16; Mismatches 25; Indels 5; Gaps 2;  
 Qy 101 THORSISPWRYRVDTDEDRYPOKLAFAECLRCICIDARTGRETAAALNSVRLQSLVLLR 160  
 Db 30 SNKRSLSPWGTSINHHDPSRIPEDLPARCLCLGCVNPFTMQRDRSNVSVVF-SQVVPVRR 88  
 Qy 161 RPCSRDGSGLPTPG 174  
 Db 89 RLCPOP---PRPG 98

RESULT 15  
 Q19778 PRELIMINARY; PRT; 148 AA.  
 ID Q19778  
 AC Q19778;  
 DT 01-NOV-1996 (TRIMBLref. 01, Last sequence update)  
 DT 01-NOV-1996 (TRIMBLref. 01, Last annotation update)  
 DT 01-DEC-2001 (TRIMBLref. 19, Last annotation update)  
 DE F25D1.3 PROTEIN.  
 GN F25D1.3.  
 OS Caenorhabditis elegans.  
 OC Eukarya; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peioderinae; Caenorhabditis.  
 NCBI\_TAXID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kelly P.F.;  
 RA Submitted (JUN-1996) to the EMBL/GenBank/DBBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode *C. elegans*: A platform for investigating biology.";  
 RT Science 282:2012-2018(1998).  
 RL EMBL: Z73973; CAA98248.1;  
 SQ SEQUENCE 148 AA; 16738 MW; ADB51F438DFB3940 CRC64;

Query Match 10.3%; Score 110; DB 5; Length 14;  
 Best Local Similarity 33.0%; Pred. No. 0.0018;  
 Matches 31; Conservative 17; Mismatches 34; Indels 12; Gaps 4;  
 Qy 103 QRSISPWRYRVDTDEDRYPOKLAFAECLRCICIDARTGRETAAALNSVRLQSLVLLR 162  
 Db 51 ERALCPWDSDRNYQESREPKLIAESTVCLC----RKSRSSTGAFCMPIVRKVPIIIRRVS 104  
 Qy 163 CSRDGSGLPTPGAFAFHTEFHVPVGCTCVLPRS 196  
 Db 105 CDR-STGL---WNYVRSTELI--TVGCHSVLPRT 132



Db	1	MTLLEGLLFITWLHTCLAHDPDSLRGHPISHGPCHYSAEELPLGQAPPHLARGAKWQ	60
Qy	61	ALPVAVSSLEAAASRGRHERRPSATTOCPVLRPEEVLEADTHORSISPMWRYRVDTDDRY	120
Db	61	ALPVAVSSLEAAASRGRHERRPSATTOCPVLRPEEVLEADTHORSISPMWRYRVDTDDRY	120
Qy	121	POKLAFAECLCRGCIDARTGRETAAALNSVRLLRRPQSDRGSGLPPGAFHT	180
Db	121	POKLAFAECLCRGCIDARTGRETAAALNSVRLLRRPQSDRGSGLPPGAFHT	180
Qy	181	EFTIHPVGCTCIVLPRSV	197
Db	181	EFTIHPVGCTCIVLPRSV	197

RESULT	2
117F_HUMAN	STANDARD;
ID	PRT;
Q96PD4 ; Q9NUE6 ; Q9EP18 ;	153 AA.
AC	
DT 01-MAR-2002 (Rel. 41, Created)	
DT 01-MAR-2002 (Rel. 41, Last sequence update)	
DT 01-MAR-2002 (Rel. 41, Last annotation update)	
DE Interleukin-17F precursor (IL-17F) (Interleukin-24) (Cytokine ML-1).	
GN IL17F OR IL24.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
NCBI_TAXID=9606 ;	
OX	
RN [1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21475830; PubMed=11591732;
RA	Starnes T., Robertson M.J., Sledge G., Kelich S., Nakshatri H.,
RA	Broxmeier H.E., Hronas R.
RA	"IL-17F, a novel cytokine selectively expressed in activated T cells
RT	and monocytes, regulates angiogenesis and endothelial cell cytokine
RT	production.";
RT	J. Immunol. 167:4137-4140(2001).
RL	
RN [2]	SEQUENCE OF 2-153 FROM N.A.
RP	SEQUENCE OF 2-153 FROM N.A.
RX	MEDLINE=21475866; PubMed=11591768;
RA	Kawaguchi M., Onuchic L.F., Liu X.-D., Essayan D.M., Schroeder J.J.,
RA	Xiao H.-Q., Liu M.C., Krishnamoorthy G., Germino G., Huang S.-K.,
RT	"Identification of a novel cytokine, ML-1, and its expression in
RT	subjects with asthma.";
RT	J. Immunol. 167:4430-4435(2001).
RL	
RN [3]	SEQUENCE OF 76-153 FROM N.A.
RP	SEQUENCE OF 76-153 FROM N.A.
RA	Almeida J.;
RA	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RL	
[4]	
RP	X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS), AND CHARACTERIZATION.

RX Published=11/24/464;  
 RA Hymowitz S.G., Filvaroff E.H., Yin J.P., Lee J., Cai L., Rissner P.,  
 RA Maruoka M., Mao W., Foster J., Kelley R.F., Pan G., Gurney A.L.,  
 RA de Vos A.M., Starovasnik M.A.;  
 RT "IL-17s" adopt a cystine knot fold: structure and activity of a novel  
 RT cytokine, IL-17F, and implications for receptor binding.;  
 EMBO J. 20:5323-5341(2001).  
 RL -1- FUNCTION: Stimulates the production of other cytokines such as IL-6, IL-8 and granulocyte colony-stimulating factor, and can regulate cartilage matrix turnover. Stimulates PBMC and T-cell proliferation. Inhibits angiogenesis.

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CC way modified. It must not be sold in any format.  
CC  
CC -!- SUBUNIT: Homodimer; disulfide-linked.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed in activated, but not resting, CD4+  
CC T cells and activated monocytes.  
CC -!- SIMILARITY: BELONGS TO THE IL-17 FAMILY.

RA Kadota K., Matsuda H.A., Ashburner M., Baralov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pessol G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldari R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombbert P., Nordin P., Ring B., Ringwald M., Rodriguez I., Saito M., Sato K., Shiba Y., Storch K.-F., Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynnshaw-Boriss A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; *Nature* 409:685-690 (2001). [5]

RP SEQUENCE FROM N.A.

RA Strausberg R.; "Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases, CC-1- FUNCTION: Stimulates the release of tumor necrosis factor alpha and IL-1-beta from the monocytic cell line THP-1 (By similarity). CC-1- SUBCELLULAR LOCATION: BELONGS TO THE IL-17 FAMILY.

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CC DR EMBL; AF184970; AA01319.1; -; DR EMBL; AF218726; AAG44135.1; -; DR EMBL; AF250309; IAK374.1; -; DR EMBL; AK003506; BAB22826.1; -; DR EMBL; BC002271; AAH02271.1; -; DR MGD; MGI:1928397; I117b.1; -; DR MGD; MGI:1928397; I117b.2; -; KW SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 180 INTERLEUKIN-17B.

FT DISULFID 121 176 BY SIMILARITY.

FT DISULFID 126 178 BY SIMILARITY.

FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 33 7 MDWPHSL -> YPTSTS (IN REF. 4).

FT CONFLICT 34 33 G -> R (IN REF. 4).

FT CONFLICT 65 34 R -> K (IN REF. 3).

FT CONFLICT 76 65 N -> T (IN REF. 3).

SQ SEQUENCE 180 AA; 20309 MW; E26F4C720019975 CRC64;

Query Match 15.7%; Score 168.5; DB 1; Length 180; Best Local Similarity 27.0%; Pred. No. 5.5e-09; Mismatches 28; Indels 33; Gaps 6;

Matches 53; Conservative 52; Similarity 29.7%; Score 165.5; DB 1; Length 177; Gaps 7;

Qy 7 LFLFLWHTCLA-HHDSLRGPHSITGPHCSAEEPLGQAPPHILLARGAKWQALPVA 65

Db 7 LFLFLAISFLAPSHPRNTKGKRKGGRPS-----PLAIGP-----HOVPLD 48

Qy 66 LVSSEASHRHERPSATTQCPVLRPEVELEAD-----THORSISPWRYRVDTD 116

Db 49 LVSRPVYARMLGNAVQLNSSEAKKCEVNLOWLWSKRSLSPWGYSINHD 108

Qy 117 EDRYPQKLAFAECLCRGCIIDARTGRTAAALNSVRLQSLVRRPCSRDGSGLPPRGAF 176

Db 109 PSRIPADLPEARCLCQCVNPETMDRSVSPVFSQVPRRLCPQP----PRPGPC 163

Qy 177 AFHTEFHIVPGCTCV 192

Db 164 RQRVVMETIAVGCTCI 179

Qy 178 AFHTEFHIVPGCTCV 192

Db 175 RQRVVMETIAVGCTCI 179

Qy 179 AFHTEFHIVPGCTCV 192

Db 180 RQRVVMETIAVGCTCI 179

Qy 181 AFHTEFHIVPGCTCV 192

Db 182 RQRVVMETIAVGCTCI 179

Qy 183 AFHTEFHIVPGCTCV 192

Db 184 RQRVVMETIAVGCTCI 179

Qy 185 AFHTEFHIVPGCTCV 192

Db 186 RQRVVMETIAVGCTCI 179

Qy 187 AFHTEFHIVPGCTCV 192

Db 188 RQRVVMETIAVGCTCI 179

Qy 189 AFHTEFHIVPGCTCV 192

Db 190 RQRVVMETIAVGCTCI 179

Qy 191 AFHTEFHIVPGCTCV 192

Db 192 RQRVVMETIAVGCTCI 179

Qy 193 AFHTEFHIVPGCTCV 192

Db 194 RQRVVMETIAVGCTCI 179

Qy 195 AFHTEFHIVPGCTCV 192

Db 196 RQRVVMETIAVGCTCI 179

Qy 197 AFHTEFHIVPGCTCV 192

Db 198 RQRVVMETIAVGCTCI 179

Qy 199 AFHTEFHIVPGCTCV 192

Db 200 RQRVVMETIAVGCTCI 179

Qy 201 AFHTEFHIVPGCTCV 192

Db 202 RQRVVMETIAVGCTCI 179

Qy 203 AFHTEFHIVPGCTCV 192

Db 204 RQRVVMETIAVGCTCI 179

Qy 205 AFHTEFHIVPGCTCV 192

Db 206 RQRVVMETIAVGCTCI 179

Qy 207 AFHTEFHIVPGCTCV 192

Db 208 RQRVVMETIAVGCTCI 179

Qy 209 AFHTEFHIVPGCTCV 192

Db 210 RQRVVMETIAVGCTCI 179

Qy 211 AFHTEFHIVPGCTCV 192

Db 212 RQRVVMETIAVGCTCI 179

Qy 213 AFHTEFHIVPGCTCV 192

Db 214 RQRVVMETIAVGCTCI 179

Qy 215 AFHTEFHIVPGCTCV 192

Db 216 RQRVVMETIAVGCTCI 179

Qy 217 AFHTEFHIVPGCTCV 192

Db 218 RQRVVMETIAVGCTCI 179

Qy 219 AFHTEFHIVPGCTCV 192

Db 220 RQRVVMETIAVGCTCI 179

Qy 221 AFHTEFHIVPGCTCV 192

Db 222 RQRVVMETIAVGCTCI 179

Qy 223 AFHTEFHIVPGCTCV 192

Db 224 RQRVVMETIAVGCTCI 179

Qy 225 AFHTEFHIVPGCTCV 192

Db 226 RQRVVMETIAVGCTCI 179

Qy 227 AFHTEFHIVPGCTCV 192

Db 228 RQRVVMETIAVGCTCI 179

Qy 229 AFHTEFHIVPGCTCV 192

Db 230 RQRVVMETIAVGCTCI 179

Qy 231 AFHTEFHIVPGCTCV 192

Db 232 RQRVVMETIAVGCTCI 179

Qy 233 AFHTEFHIVPGCTCV 192

Db 234 RQRVVMETIAVGCTCI 179

Qy 235 AFHTEFHIVPGCTCV 192

Db 236 RQRVVMETIAVGCTCI 179

Qy 237 AFHTEFHIVPGCTCV 192

Db 238 RQRVVMETIAVGCTCI 179

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Qy 597 AFHTEFHIVPGCTCV 192

Db 598 RQRVVMETIAVGCTCI 179

Qy 599 AFHTEFHIVPGCTCV 192

Db 600 RQRVVMETIAVGCTCI 179

Qy 601 AFHTEFHIVPGCTCV 192

Db 602 RQRVVMETIAVGCTCI 179

Qy 603 AFHTEFHIVPGCTCV 192



33b 123 BREPPHCPN-----SEBIEKTIYSVGCCTCVTBP 149

IL17B OR NIFR.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Cricetinae;  
 OC NCBI\_TaxID=1036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Moore E.E., Presnell S., Garrigues U., Guibot A., LeGuern E.,  
 RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;  
 RT "Identification of a novel IL-17 related factor: demonstration of  
 neuronal expression and evaluation as a candidate for the chromosome  
 5q-linked form of Charcot-Marie-Tooth disease.";  
 RT Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
 RL -;  
 CC FUNCTION: Stimulates the release of tumor necrosis factor alpha  
 CC and IL-1beta from the monocytic cell line THP-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Belongs to the IL-17 family.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; AF218725; AAG44134.1; -;  
 KW Cytokine; Glycoprotein; Signal.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 >178 INTERLEUKIN-17B.  
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT DISULFID 121 176 BY SIMILARITY.  
 FT DISULFID 126 178 BY SIMILARITY.  
 FT NON-TER 178 178  
 SQ SEQUENCE 178 AA; 2007 MW; 03D02D60BEC89A51 CRC64;  
 -----  
 Query Match 14.7%; Score 157.5; DB 1; Length 178;  
 Best Local Similarity 29.5%; Pred. No. 5.9e-08; 4;  
 Matches 46; Conservative 23; Mismatches 70; Indels 17; Gaps  
 -----  
 Qy 45 GQAPPHILLARGAKWQGQALPVAVSSLEAAHSRGRHERPSATTQCPVLRPEELEAD--- 100  
 Db 31 GQVPRGPGLGP - -HOVPLDLSVRYKPYARMEEYERNLGMVAQLRNSSEPAKRRCEVN 87  
 Qy 101 ---T-THORSISPWRYVTDTEDRYDPOQLKAFAECLCRGCIIDARTGRETAAINSVRLQSL 155  
 Db 88 LOLWLWNSKRLSPWPWGSINHDSRIPADLPEARCLCLGCVNPFETMOEDRSMVSPVFSQ 146  
 Qy 156 LVYRRRRPSCRSQGSLGLPPGAGAFHTERIHYPVGCTC 191  
 Db 147 VPVRRRLCPPP---PRPGPCRHRVYMETAVGCTC 178  
 -----  
 RESULT 9  
 117B\_HUMAN STANDARD; PRT; 180 AA.  
 ID 117B\_HUMAN STANDARD; PRT; 180 AA.  
 AC Q9UHF5;  
 DT 01-MAR-2002 (Rel. 41, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DE Interleukin-17B precursor (IL-17B) (Cytokine-like protein ZCYT07)  
 DE (Neuronal interleukin-17 related factor) (Interleukin-20).  
 GN IL17B OR ZCYT07 OR NIFR OR IL20.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Presnell S.; Gilbert T.; Whitmore T.; Foster D.; Hart C.; Lehner J.;  
 RA Martinez T.; Hoffman R.; O'Hara P.;  
 RA NCBI\_TaxID=1036;



FT CONFLICT 46 46 I  $\rightarrow$  L (IN REF. 3).  
 SQ SEQUENCE 150 AA; 16876 MW; EF133EDF9D689F CRC64;

Query Match 13.8%; Score 148.5; DB 1; Length 150;  
 Best Local Similarity 29.4%; Pred. No. 3.4e-07;  
 Matches 45; Conservative 20; Mismatches 55; Indels 33; Gaps 5;

Qy 42 LPLGQAPPHLARGKKGQALPVALVSSLEASHRGRHERRPSATTQCPVLRPEEVEADT 101  
 Db 21 IPQSSVCPNAEANNFLQVNKVNLKINSL--SSKASSRRPS-----D 61

Qy 102 HORSTSPWRYRVDTDEDYPOKLAFACLRCGTCIDARTGRTAAALNSVRLQSLLVRR 161  
 Db 62 LNRSTSPWTLRSRNEDDYPSPVTLRNSVLLQETILVKE 120

Qy 162 P--CSRDGSGLPLTPGAFAFHTEFHYPVGCTV 192  
 Db 121 PEKC-----PTEFVKEKMLVGVGCTV 142

Db 119 QQEILVLRKREFES-----CPPTFRVERMLVGVGCTV 150

RESULT 12

HNF6\_HUMAN  
 ID HNF6\_HUMAN STANDARD; PRT; 465 AA.  
 AC Q99744;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hepatocyte nuclear factor 6 (HNF-6) (One cut domain family member 1).  
 GN ONECUT1 OR HNF6A OR HNF6.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Furuta H., Horikawa Y., Wang Y.-Q., Bell G.I.;  
 RT "Isolation and characterization of the human hepatocyte nuclear factor  
 6 gene.";  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Furuta H., Wang Y.-Q., Bell G.I.;  
 RT "The sequence of human mRNA for the hepatocyte nuclear factor  
 alpha-1.";  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 1-368 FROM N.A., AND VARIANT ALA-75.  
 RX MEDLINE=99z20592; PubMed=10491763;  
 RA Moeller A.M., Ek J., Durvila S.A., Urhammer S.A., Clausen J.O.,  
 RA Biberg H., Hansen T., Rousseau G.C., Lemaigne F.P., Pedersen O.,  
 RT "Hepatocyte nuclear factor-6: associations between genetic variability  
 and type II diabetes and between genetic variability and estimates of  
 insulin secretion.";  
 RT Diabetologia 42:1011-1016(1999).  
 RL SEQUENCE OF 174-465 FROM N.A.  
 RX MEDLINE=96194901; PubMed=8654948;  
 RA Yao Z., Timour M., Painter S., Fanslow W., Spriggs M.K.;  
 RT "Complete nucleotide sequence of the mouse CTIA8 gene.";  
 RL Gene 168:223-225(1996).  
 CC FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND  
 CC HEMATOPOIETIC CYTOKINES (BY SIMILARITY).  
 CC 1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC 1- SUBCELLULAR LOCATION: RESTRICTED TO A SUBSET OF ACTIVATED T-CELLS.  
 CC 1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
 CC 1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE  
 CC 5'-DHWATGATWWD-3', ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE  
 CC OF HNF3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION.  
 CC 1- SUBUNIT: BINDS DNA AS A MONOMER (BY SIMILARITY).  
 CC 1- SUBCELLULAR LOCATION: Nuclear.  
 CC 1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER; LOWER EXPRESSION IN  
 CC TESTIS AND SKIN.  
 CC 1- SIMILARITY: CONTAINS 1 CUT DOMAIN.  
 CC 1- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEOPBOX PROTEINS.

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 CC 1- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEOPBOX PROTEINS.

CC DR EMBL: U35108; AAA93253.1; .  
 DR MGI:107364; IL17.  
 KW Cytokine; Glycoprotein; T-cell; Antigen; Signal.  
 FT SIGNAL 1 25 POTENTIAL  
 FT CHAIN 26 158 INTERLEUKIN-17.  
 FT DISULFID 97 147 BY SIMILARITY.

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CC Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE

CC 5'-DHWATGAYTWMD-3' ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE

CC OF HNF3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION (BY

CC SIMILARITY).

CC -!- SUBUNIT: BINDS DNA AS A MONOMER (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- SIMILARITY: CONTAINS 1 CUT DOMAIN.

CC -!- SIMILARITY: BELONGS TO THE CUT DOMAIN OF HOMEOBOX PROTEINS.

CC

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CC

DR EMBL: U95945; AAB3863\_1; - .

DR TRANSFAC; T0296; - .

DR MGDB; MG1:1196423; OneCut1.

DR InterPro; IPR003350; CUT.

DR InterPro; IPR01356; Homeobox.

DR Pfam; PF02376; CUT.

DR Pfam; PF00046; homeobox; 1.

DR SMART; SM00389; HOX; 1.

DR PROSITE; PS00027; HOMEOBOX\_1; FALSE\_NEG.

DR PROSITE; PS50071; HOMEOBOX\_2; 1.

KW transcription regulation; Homeobox; DNA-binding; Nuclear protein;

KW Activator; Polymorphism.

DNA\_BIND 283 369 CUT.

DNA\_BIND 385 444 HOMEOBOX.

FT DOMAIN 69 72 POLY-HIS.

FT DOMAIN 124 138 POLY-HIS.

FT DOMAIN 455 460 POLY-SER.

FT VARIANT 75 75 P->A.

FT CONFLICT 220 220 /FTID=VAR\_010729.

FT CONFLICT 284 284 A->T (IN REF. 3 AND 4).

FT CONFLICT 288 288 S->N (IN REF. 4).

FT CONFLICT 318 318 Q->H (IN REF. 4).

FT CONFLICT 386 386 R->K (IN REF. 4).

FT CONFLICT 51023 MW; F47F78957A6ECFC2 CRC64;

SEQUENCE 465 AA; 465 AA; Score 85.5; DB 1; Length 465; Best Local Similarity 25.8%; Pred. No. 1; Mismatches 14; Gaps 11; Matches 48; Conservative

Query Match 18 AHHDPSLRGHPHSHGTPHCKYSAEELPGQAPP----HLLARGAKNGQALPVYSSLEA 72

Matches 220 AHPAMIGRGRHGEHLP-TSAGMVPINGLPPPHAHLNAGG--HGQLLSTA-----268

Qy 73 ASHRGRHERPSAT-----REPNSVTGAQVNSNGNSGQMEINTEKVAQ-----RITTELKRYSI 310

Db 269 ---PQKLAFAECLCR--GCID-----ARTGRETAAALNSVRL-----LQSLIVLR 159

Qy 121 PQKLAFAECLCR--GCID-----ARTGRETAAALNSVRL-----LQSLIVLR 159

Db 311 PQAFIAQRVLCRSGTQLSLRNPKPKNSKLSGRETER---RMWKWLQEEPEFORMSALR 366

Qy 160 RRPCSR 165

Db 367 LAACKR 372

RESULT 13 HNF6\_MOUSE STANDARD; PRT; 465 AA.

AC 008755; HNF6\_MOUSE STANDARD; PRT; 465 AA.

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hepatocyte nuclear factor 6 (HNF-6) (One cut domain family member 1).

DE ONECUT1 OR HNF6 OR HNF6.

OS Mus musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus

OX NCBI\_TaxID=10090; Rattus norvegicus (Rat).

RN RSEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Samadani U., Rausa F., Costa R. H.; "Mouse hepatocyte nuclear factor-6 cDNA."



RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Weissbach H., Wu D., Yang S.-S., Yao Q.A., Zhang J., Zhang K.C., Zhang L., Ye J., Yeh R.-F., Zaveri J.S., Zhang M., Zhao Q., Zheng L., Zhang H., Zhang X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbons R.A., Myers E.W., Rubin G.M., Venter J.C., Venter J.C., RT "The genome sequence of *Drosophila melanogaster*," RT Science 287:2185-2195 (2000).  
 RL -!- FUNCTION: MAY ACT AS COACTIVATOR, ASSISTING ONE OR MORE DEDICATED TRANSCRIPTIONAL ACTIVATORS OF ANT-C AND BX-C HOMEBOTIC GENES. CAN COUNTERACT THE REPRESSIVE EFFECT OF POLYCOMB PROTEIN.  
 CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -!- DEVELOPMENTAL STAGE: HIGHEST EXPRESSION IN UNFERTILIZED EGGS AND EARLY EMBRYOS.  
 CC -!- MISCELLANEOUS: 'BRAHMA' MEANS 'FATE' IN INDIA.  
 CC -!- SIMILARITY: CONTAINS 1 BROMODOMAIN.  
 CC -!- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.  
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 CC DR EMBL; M85049; AAA19661.1; .  
 CC DR EMBL; AE003529; AAF49557.1; .  
 CC DR EMBL; AE003529; AAF49558.2; .  
 CC DR FLYBase; FBan000212; brm.  
 CC DR InterPro; IPR001487; Bromodomain.  
 CC DR InterPro; IPR001410; DEAD.  
 CC DR InterPro; IPR001650; Helicase\_C.  
 CC DR InterPro; IPR000330; SNF2\_N.  
 CC DR PF00439; bromodomain\_1.  
 CC DR Pfam; PF00271; helicase\_C; 1.  
 CC DR Pfam; PF00176; SNF2\_N; 1.  
 CC DR SMART; SM00503; BROMODOMAIN.  
 CC DR SMART; SM00297; BROMO; 1.  
 CC DR SMART; SM00490; HELIC; 1.  
 CC DR PROSITE; PS00633; BROMODOMAIN\_1; 1.  
 CC DR PROSITE; PS00014; BROMODOMAIN\_2; 1.  
 CC KW Activator; Bromodomain; Transcription; Nuclear protein;  
 CC FT DOMAIN 201 390 GLN/PRO RICH.  
 CC FT SITE 900 903 DESH BOX.  
 CC FT DOMAIN 1385 1392 ASP/GLU RICH (ACIDIC).  
 CC FT DOMAIN 1394 1404 ARG/LYS RICH (BASIC).  
 CC FT DOMAIN 1405 1410 ASP/GLU RICH (ACIDIC).  
 CC FT DOMAIN 1415 1432 ARG/LYS RICH (BASIC).  
 CC FT DOMAIN 1443 1453 BROMODOMAIN.  
 CC FT DOMAIN 1631 1638 POLY-ASP.  
 CC FT VARSPLIC 121 121 G -> A (IN SHORT ISOFORM).  
 CC FT VARSPLIC 122 222 MISSING (IN SHORT ISOFORM).  
 CC FT CONFLICT 687 687 D -> Y (IN REF.).  
 CC SQ SEQUENCE 1638 AA; 185088 MW; A4494B29F4F2B42A CRC64;

Query Match 7.93; Score 84.5; DB 1; Length 1638;  
 Best Local Similarity 22.28; DB 1; Length 1638;  
 Matches 42; Conservative 26; Mismatches 70; Indels 51; Gaps 8;  
 Qy 22 PSLRGPHPHSHGTPHCVSAEELPLGQAPPH---LLARGKQGQALPVAVLSLEASHRG 77  
 Db 52 PGAYGHPMQHGP---GQGPGHMPHMPHQGMIFSKHGMQMP---PTGPNNSPYQT 104  
 Qy 78 RHERPSATTOCPVLR-----PEEVLADTH---QRSISPVWRYRVDTDEDRYPKQLA 125  
 Db 105 HGMPNPAQTQPCIVSPGPGPPERSSSOENLHALQRAIDSMEEBKLQDPRTSQLA 164

GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd.												
MM protein - protein search, using sw model												
run on:	August 23, 2002, 16:00:54 : Search time 19.69 Seconds (without alignments) 961.381 Million cell updates/sec											
title:	US-09-854-208-3											
perfect score:	1073											
sequence:	1 MLLPGLLFLTWLHTCLAHH..... FHTEF1HVPVGCTVLPRTSV 197											
scoring table:	BLOSUM62											
searched:	283138 seqs, 96089334 residues											
total number of hits satisfying chosen parameters: 283138												
minimum DB seq length: 0												
maximum DB seq length: 2000000000												
post-processing: Minimum Match 0%												
Maximum Match 100%												
Listing first 45 summaries												
database :	PIR_71;*											
	1: pir1;*											
	2: pir2;*											
	3: pir3;*											
	4: pir4;*											
Pred. No. is the number of results predicted by chance to have a												
score greater than or equal to the score of the result being printed,												
and is derived by analysis of the total score distribution.												
SUMMARIES												
result No.	Score	Query Match	Length	DB ID	Description							
1	160.5	15.0	151	1 B45351	immediate-early pr							
2	148.5	13.8	147	2 JC4628	cytotoxic T-lympho							
3	148.5	13.8	150	2 I49623	cytotoxic T-lympho							
4	110	10.3	148	2 T21334	hypothetical prote							
5	93.5	8.7	395	1 KISMG	galactokinase (BC)							
6	86.5	8.1	389	2 T50809	hypothetical prote							
7	86	8.0	297	2 JL0032	hypothetical prote							
8	84.5	7.9	1638	2 A42091	hypothetical acti							
9	82.5	7.7	635	2 S76371	hypothetical prote							
10	81.5	7.6	735	2 T23218	hypothetical prote							
11	81	7.5	553	2 D83640	hypothetical prote							
12	80.5	7.5	210	2 B40203	hypothetical prote							
13	80	7.5	411	2 A70509	4-alpha-glucanotra							
14	79.5	7.4	638	2 JC7753	hypothetical prote							
15	79	7.4	549	2 T37386	ring finger B-box							
16	79	7.4	837	2 T12514	fas-activated seri							
17	79	7.4	885	2 S75894	ethylene-insensit							
18	78.5	7.3	132	2 E72603	fxud protein - Myc							
19	78	7.3	309	2 T37033	replication initia							
20	77.5	7.2	209	2 T30698	beta-N-acetylhexos							
21	77.5	7.2	323	2 A35909	3-hydroxy-3-methyl							
22	77.5	7.2	567	2 E96764	pre-mRNA splicing							
23	77	7.2	420	2 T14166	hypothetical prote							
24	77	7.2	466	2 T36212	hypothetical prote							
25	77	7.2	639	2 F97670	hypothetical prote							
26	77	7.2	639	2 AC2895	hypothetical prote							
27	76.5	7.1	405	2 G84338	fra-2 protein - ch							
28	76.5	7.1	503	2 S64787	ethylene-insensit							
29	76.5	7.1	1882	2 T00069	fxud protein - Myc							

RESULT 2  
 JC4628 cytoxic T-lymphocyte-associated antigen 8 precursor - mouse  
 N:Alternate names: CtlA8 protein  
 C:Species: Mus musculus (house mouse)  
 C:Accession: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
 R:Rao, Z.; Timour, M.; Painter, S.; Fanslow, W.; Spriggs, M.  
 A:Title: Complete nucleotide sequence of the mouse CTLA8 gene.  
 A:Reference number: JC4628; MUID: 96194901  
 A:Molecule type: DNA  
 A:Residues: 1-147 <YAO>  
 A:Cross references: GB:U035108; NID:91244499; PIDN:AAA93253.1; PID:91244500  
 C:Genetics:  
 A:Gene: ctl8  
 A:Introns: 69/2  
 C:Superfamily: saimiri herpesvirus immediate-early protein 2  
 C:Keywords: cytokine; glycoprotein; lymphocyte  
 F:1-147/Domain: signal sequence #status predicted <STG>  
 F:15-147/Domain: cytotoxic T-lymphocyte-associated antigen 8 #status predicted <MAT>  
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.8%; Score 148.5; DB 2; Length 147;  
 Best Local Similarity 37.6%; Pred. No. 1.5e-06;  
 Matches 38; Conservative 13; Mismatches 35; Indels 15; Gaps 3;  
 Qy 92 RPEBEVADTHORSISPPWRYRVDTPDRYDPOQKLAFAECLCRGCTIDARTGRTAAALNSVRL 151  
 Db 54 RPSDYL----NRSTSPWTLHARNEDPDRYPSVWEACRQRCVNNE-GKLDHHMNSVLI 107  
 Qy 152 LQSLVLLRRPCSRDGSGLPPTGAFAHTEFTHPVGCTCY 192  
 Db 108 QQEILVLRREPES-----CPFTFVERKMLVGVGTCTV 139

RESULT 3  
 I49623 cytoxic T-lymphocyte-associated antigen 8 precursor - mouse  
 N:Alternate names: immediate-early protein 2 (ORF13) homolog  
 C:Species: Mus musculus (house mouse)  
 C:Accession: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 26-Aug-1999  
 R:Rouvier, E.; Luciani, M.  
 J: Immunol. 150, 5445-5456, 1993  
 A:Title: CtlA-8, cloned from an activated T cell, bearing AU-rich messenger RNA instability  
 A:Reference number: I49623; MUID: 93294300  
 A:Accession: I49623  
 A:Molecule type: mRNA  
 A:Residues: 1-150 <RES>  
 A:Cross references: GB:L13839; NID:9293329; PIDN:AAA37490.1; PID:9293330  
 C:Genetics:  
 A:Gene: CtlA-8  
 C:Superfamily: saimiri herpesvirus immediate-early protein 2

Query Match 13.8%; Score 148.5; DB 2; Length 150;  
 Best Local Similarity 29.4%; Pred. No. 1.5e-06;  
 Matches 45; Conservative 20; Mismatches 55; Indels 33; Gaps 5;  
 Qy 42 IPLGQAPHILARGAKWQALPVAVSSLEAASHRGRHRSATTCQCPVLRPEEVELEADT 101  
 Db 21 IFOSSYCPNAANFLQNVKLNKLNSL---SSKASSRRES-----DY 61  
 Qy 102 HORSISPPWRYRVDTPDRYDPOQKLAFAECLCRGCTIDARTGRTAAALNSVRLQSLIYLRR 161  
 Db 62 INRSTSWTLLSRNEDDRYPSVWEACRQRCVNNE-GKLDHHMNSVLIQEQEILVLR 120  
 Qy 162 P-CSRDGSGLPPTGAFAHTEFTHPVGCTCY 192

RESULT 4  
 T21334 hypothetical protein F25D1.3 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Accession: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 R:Kelly, P.  
 submitted to the EMBL Data Library, June 1996  
 A:Reference number: T21334  
 A:Accession: T21334  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-148 <WIL>  
 A:Cross references: EMBL:Z73973; PIDN:CAA98268.1; GSPDB:GN00023; CESP:F25D1.3  
 A:Experimental source: clone F25D1  
 C:Genetics:  
 A:Gene: CESP:F25D1.3  
 A:Map position: 5  
 A:Introns: 60/2

Query Match 10.3%; Score 110; DB 2; Length 148;  
 Best Local Similarity 33.0%; Pred. No. 0.0054;  
 Matches 31; Conservative 17; Mismatches 34; Indels 12; Gaps 4;  
 Qy 103 ORSISPPWRYRVDTPDRYDPOQKLAFAECLCRGCTIDARTGRTAAALNSVRLQSLIYLRR 162  
 Db 51 ERAICPDPDSRVNQESREPKLIAESVLC----RKSRSSTGAFCMPIVRKVPILRRS 104  
 Qy 163 CSRDSGSGLPPTGAFAFTEFTHPVGCTCYLPRS 196  
 Db 105 CDR-STGL---WNYVRSRTELI--TVGCHSVLPLRT 132

RESULT 5  
 K1SMG galactokinase (EC 2.7.1.6) - Streptomyces sp.  
 C:Species: Streptomyces sp.  
 C:Accession: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 28-May-1999  
 R: Adams, C. W.; Fornwald, J. A.; Schmidt, F. J.; Rosenberg, M.; Brawner, M. E.  
 J: Bacteriol. 170, 203-212, 1988  
 A:Title: Gene organization and structure of the Streptomyces lividans gal operon.  
 A:Reference number: A28669; MUID:88066869  
 A:Accession: C28669  
 A:Molecule type: DNA  
 A:Residues: 1-395 <ADA>  
 A:Cross references: GB:MI1953; NID:9153259; PIDN:AAA26748.1; PID:9153262  
 A:Note: the source is designated as Streptomyces lividans  
 C:Genetics:  
 A:Gene: galk  
 C:Superfamily: galactokinase  
 C:Keywords: ATP; galactose metabolism; phosphotransferase

Query Match 8.7%; Score 93.5; DB 1; Length 395;  
 Best Local Similarity 29.5%; Pred. No. 0.53;  
 Matches 44; Conservative 15; Mismatches 79; Indels 11; Gaps 5;  
 Qy 32 GTPHCYSAAEPLQGQAPHILARGK-ARW---GQALPVAVSSLEAASHRGRHRSATTCQCPVLRPEEVELEADT 86  
 Db 183 GTPSSSTPATSDSGRDPSTSPPRGCAQWSSTPGSSTPATARSTASARAARRAPRCWAST 242  
 Qy 87 QC--PVLRPEEVELEADTHORSISPPWRYRVDTPDRYDPOQKLAFAECLCRGCTIDARTGRTAAALNSVRLQSLIYLRR 161  
 Db 243 RCDVPTADLDAELERLQDDEEVRLRVWVTEDEVERVVALLESATPGASAPSMSRATP 302  
 Qy 145 ALNSVRLQSLIYLRRPCSRDGSGLPPTP 173

Db	303 A---ARRLPHLIP-RAGPGRHGPGLRGP	327	Qy	48 PPHLARGAKWGOALPVAL-----VSSLEAASH-----RGRHERPSA-----TTQ 87
RESULT	6		Db	28 PSRLILLLG---WNRPAVLQDQLRSTARQSSEVVAAPGPRGTDROPAGRDRYRFRQ 85
T50809	hypothetical protein T30N20_270 - Arabidopsis thaliana		Qy	88 CPVLRPEEVLEADTHQRS---TSPWRYRVDTDEDRYPKQLAFACELORGCIDARQRET 143
C;Species:	Arabidopsis thaliana (mouse-ear cress)		Db	86 APLSRPTEVIGLDLDRYDAVYVLPDR---GDGPDHDDWTLVAVRLDDGRTGRET 141
C;Date:	21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000		Qy	144 AALNSVRLQSLIULRRPCSRDGS 169
C;Accession:	T50809		Db	142 -----RVVTELVDDRNRLAPVNSG 161
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; New				
submitted to the Protein Sequence Database, July 2000				
A;Reference number:	Z25240			
A;Accession:	T50809			
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-389 <BEV>				
A;Cross references: EMBL:AL365234				
A;Experimental source: cultivar Columbia; BAC clone T30N20				
C;Genetics:				
A;Map position: 5				
A;Note: T30N20_270				
Query Match	8.1%	Score 86.5; DB 2; Length 389;		
Best Local Similarity	23.0%	Pred. No. 2, 3;		
Matches 56; Conservative 25; Mismatches 83; Indels 79; Gaps 10;				
Qy	6 GLLFITWLHTCLAHHDLSLRGIP---HSHGTHCHYCAEELPGQAPP-HL---LA--- 53			
Db	44 GVFYLIMSRFLGGHSYNFLHSQDYNHNSPPLFSSADLSLSSAYSFHLNINTLAFWK 103			
Qy	54 RGAK-----WG-----QALPVAV-----SSLEASHRGRHER 81			
Db	104 PSATTQCPVLRPEEVLEADTHDRSISPVWRYDTPDDEPYPKLAFACELRCGICDAR-- 138			
Qy	82 SVDSKVQVLRQIKRLRKFRGNEKVEIDGVHVOISWDVYNNWLFQSKSSGDGGGGHAVMF 271			
Db	164 PPTNPQALLRKKEHFGA-----RVFTTKAREGGKRNREISIDCRVDEDAKLKF 211			
Qy	139 -----TGTRETAALNSVRLQSLIULRRPCSRDGSGLPPTPAAFAV 178			Query Match 7.9%; Score 84.5; DB 2; Length 1638;
Db	212 SVDSKVQVLRQIKRLRKFRGNEKVEIDGVHVOISWDVYNNWLFQSKSSGDGGGGHAVMF 271			Best Local Similarity 22.2%; Pred. No. 17;
Qy	179 HTE 181			Matches 42; Conservative 26; Mismatches 70; Indels 51; Gaps 8;
Db	272 RFE 274			
RESULT	7		Qy	22 PSLRGHPISHGTPHCYSAEELPLGQAPPH---LLARGAKNGQALPVAVLSSLEASHRG 77
JL0032	hypothetical 31.7K protein (aphE region) - Streptomyces griseus		Db	52 PGAYGHPKHQHGPDP---GGGPQHMPHQQMIFSGPHMOMP---PRGPNMSPYQT 104
C;Species:	Streptomyces griseus		Qy	78 RHERPSATTQCPVLR-----PEEVLEADTH---QRSISPVWRYDTPDDEPYPKLA 125
C;Sequence_revision:	31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Oct-1999		Db	105 HGMPNAPTOQPCIVSPGGPPGGPPPERSSOENLHALQRATDSMEERGLOEDPRYSQLLA 164
C;Accession:	JL0032		Qy	126 FAECLRCGICDARTGREAALNSVRLQS---LVLRRRPCSRD----- 166
A;Title: A second streptomycin resistance gene from Streptomyces griseus codes for strep			Db	165 -----MRATSKHQHNGQVNLLRTQTAYRLLARNKPTSMQMQQALQAQQQPPP 215
A;Reference number:	JL0031; MUID:88339496		Qy	167 GSGLPLTPGA 175
A;Accession:	JL0032		Db	216 GPPIGPPGA 224
A;Molecule type: DNA			RESULT	9
A;Residues: 1-297 <HEV>			S76371	hypothetical protein - <i>Synechocystis</i> sp. (strain PCC 6803)
A;Cross references: GB:M37378; NID:9153162; PIDN:AAA26701.1; PID:9153164			C;Species: <i>Synechocystis</i> sp.	
A;Experimental source: strain N2-3-11			A;Variety: PCC 6803	
C;Genetics:			C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000	
A;Gene: orf1			C;Accession: S76371	
C;Superfamily: Streptomyces griseus hypothetical 31.7K protein (aphE region)			R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas	
Query Match	8.0%	Score 86; DB 2; Length 297;	DNA Res.	DNA Res. 3, 109-136, 1996
Best Local Similarity	27.4%	Pred. No. 1, 9; Mismatches 15; Indels 36; Gaps 7;	A;Title: Sequence analysis of the genome of the unicellular cyanobacterium <i>Synechocystis</i>	
Matches 40; Conservative 15; Mismatches 15; Indels 36; Gaps 7;			A;Reference number: S74322; MUID:97061201	
			A;Accession: S76371	



**RESULT** 13  
 A70509 hypothetical protein Rv1230c - *Mycobacterium tuberculosis* (strain H37RV)  
 C;Species: *Mycobacterium tuberculosis*  
 C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
 C;Accession: A70509  
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998  
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome  
 A;Reference number: A70500; MUID:98265987  
 A;Accession: A70509  
 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-411 <COL>  
 A;Cross-references: GB:928260; GB:AL123456; NID:93261826; PIDN:CAB10927.1; PID:e1299939;  
 A;Experimental source: strain H37RV  
 C;Genetics:  
 C;Gene: Rv1230c

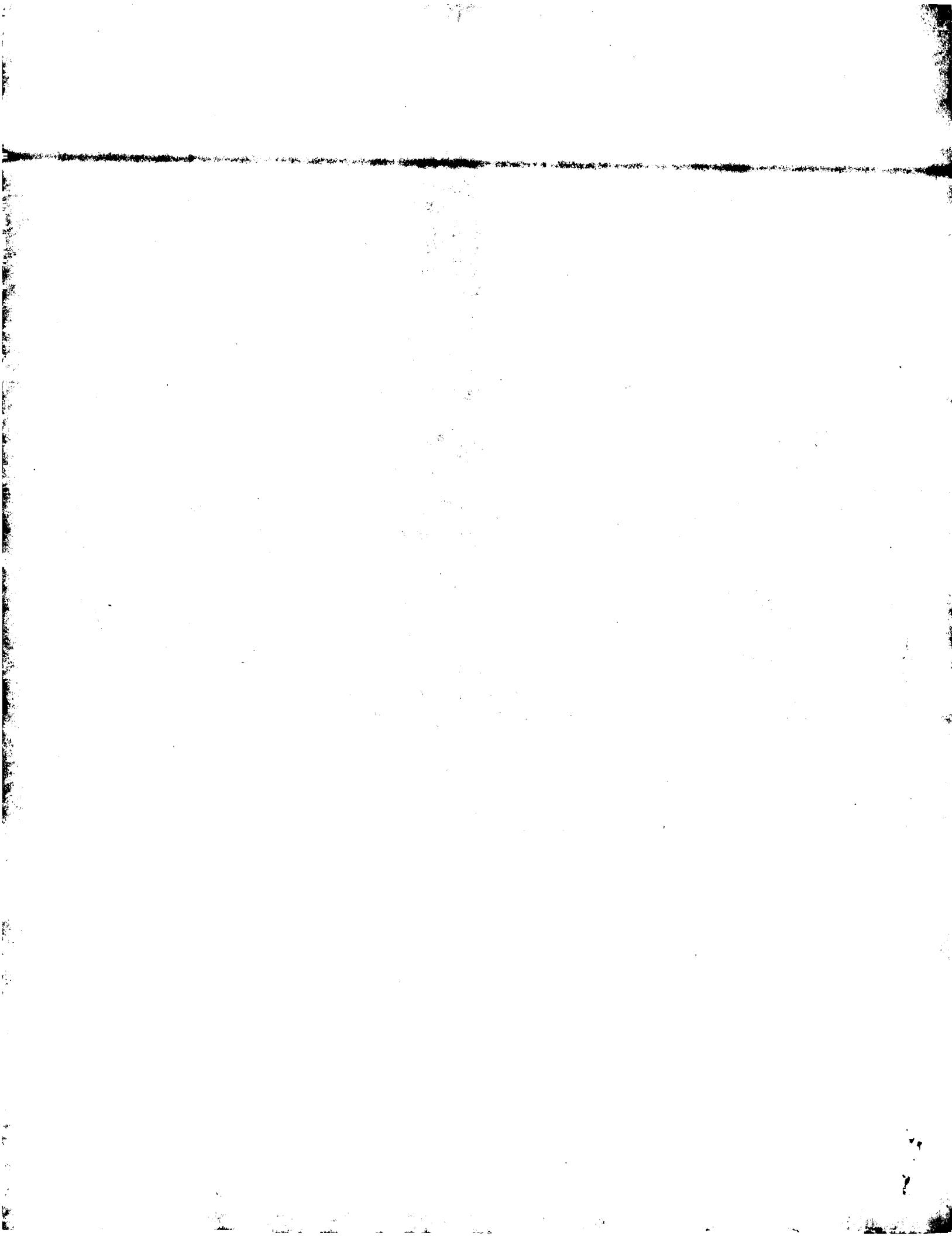
Query Match	7.5%	Score 80;	DB 2;	Length 411;
Best Local Similarity	23.7%	Pred. No. 9	8;	
Matches	45;	Conservative	23;	Mismatches 78;
				Indels 44;
				Gaps 10;
Qy	5	PGLLFLTWLHTCLAHHDPSLQRGHPHSHGTP	---	HCYSAEELPLIGQAPPHLARGAKWQGQ 60
Db	85	PPTSFRAVATISAPPMMVNPSPGALGI	PAMALSA	YRNELKMAAAAP
		YRNELKMAAAAP	---	---GCGVSPNL 141
Qy	61	ALPVALVSSLEASHRORHERSATTOCPVLRP	---	---
		---	---	BEVLEAD
		---	---	---THQRSI 106
Db	142	LAGIGRIESMHA	---	NGGATDARGTAIOPPIYK
		---	---	PLDGTLPGNHLIIQSVGNRVTYARM 198
Qy	107	SP	---	W-RYRVDID
		---	---	---
		---	---	RYPOKLAFAEC
		---	---	CLCRGCIDARTGRET
		---	---	-AAL
		---	---	---
Db	199	GPMQFLPGTWAYATGDDGVADPQNLF	DSTLAAARYLCSGGNLNRDPAQYMAALLRYN	258
Qy	147	NSVRLQSLI	156	
Db	259	NSMPYFAQNV	1	268

RESULT 14  
 JC7753 ring finger B-box coiled-coil protein, GOA - human  
 C:Species: Homo sapiens (man)  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 14-Dec-2001  
 C:Accession: JC7753  
 R:Vandeputte, D.A.; Meijer, C.B.; van Dartel, M.; Leenstra, S.; IJlst-Keizers, H.; Das, Biochem. Biophys. Res. Commun. 286, 574-579, 2001  
 A:Title: GOA: a novel gene encoding a ring finger B-box coiled-coil protein, is overexpressed  
 A:Reference number: JC7753; MUID:21402356; PMID:11511098  
 A:Accession: JC7753  
 A:Molecule type: DNA  
 A:Residues: 1-658 <WAN>  
 A:Cross-references: GB:AY026563  
 C:Comment: This protein, a member of the subfamily of the ring finger proteins, has an i

Query	40	EELPQQAPHILLARGAKWGNALPVAL-	VSSLEA-	ASHRGRHERPSATTQCPVLRPDE	95
Match	7.4%	Score 79	5;	DB 2;	Length 638;
Best Local Similarity	30.3%	Pred. No. 18;			
Matches	36;	Conservative	10;	Mismatches	56;
				Indels	17;
				Gaps	6;
Qy	1118	EPWPAGEEP- : VRCDACPRGAIPAAALSCUSCASCOPAHG	GHEERSDIALRGHRIVDPLR		175
D <sub>b</sub>					

	RESULT	15
Qy	96	VLEADTHQRSLSPWYRKYDFTDDEDRYFQKLAFACFLCRCG - IDARTGRETAAINSVRLQ 153
	176	RLEESLCPRHLRPL - ERYCR - AERVCLCEAACAOERHGHELVPLQEQRALQ 224
Db		
Qy	137386	fas-activated serine/threonine kinase - human
C; Species:	Homo sapiens (man)	
C; Date:	12-Aug-1996	#text_change 21-Jul-2000
C; Accession:	I37386	
A; Tian, Q.; Taidjin, J.; Elledge, S.; Robertson, M.; Anderson, P.		
J. Exp. Med. 182, 865-874, 1995		
A; Title: fas-activated serine/threonine kinase (FAST) phosphorylates TIA-1		
A; Reference number: I37386; MUID:95378805		
A; Accession: I37386		
A; Status: preliminary; translated from GB/EMBL/DBJ		
A; Molecule type: mRNA		
A; Residues: 1-519 <RBS>		
A; Cross-references: EMBL:X86779; NID:9100665B; PIDN:CAA60448.1; PID:g100666		
C; Genetics:		
A; Gene: fast		
C; Superfamily: human fas-activated serine/threonine kinase		
Query Match	7.48;	Score 79; DB 2; Length 549;
Best Local Similarity	28.6%;	Pred. No. 1/1;
Matches	56;	Conservative 12; Mismatches 58; Indels 70; Gaps
Qy	13 LHTCLAHHDPSLRLGPHSHGTPHCYSAEE -	-LPLQGQAPPHLARGKKGQALPVA----- 65
Db	158 IHVCL -HLAVLGLFP -SDGFLVCALEQERRRLPKPKPPPLQPLRGGQGLEAAALSCPR 214	
Qy	66 -----LYSSL-EA-----	-ASHRGHRHRSATTQCPVLRPEEVLEADTH- 102
Db	215 FLRYPHQHLLSSLAEARPEELTPHYNVLLGHALARL-----	-LREPOLLEIAJAHF 264
Qy	103 -----QRTSPW --R-YRVDTDEDRYPQKLAFACFLCRCGIDARTGRETAA 146	
Db	265 LVVQETQLSKSKVYQKLVLPFGRLNW -----LPLEQQFMPCLER -ILAREA-GVAPL 313	
Qy	147 NSVRLQSSLVLRP 162	
Db	224 Amtvmtmccordvpr 220	

Search completed: August 23, 2002, 16:02:16  
Job time: 82 sec



GenCore version 4.5  
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DM protein - protein search, using sw model

Run on: August 23, 2002, 16:04:49 ; Search time 13.09 Seconds  
(without alignments)  
367.597 Million cell updates/sec

Title: US-09-854-208-3  
perfect score: 1073  
Sequence: 1 MTLLPGILFLWLHTCLAHH,.....FHTEFIHVPVGCTCVLPRSV 197

Scoring table: ~ BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*

3: /cgn2\_5/ptodata/2/iaa/6A\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/iaa/PCRTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	173	16.1	153	1 US-08-514-04-12	Sequence 12, Appl
2	173	16.1	153	2 US-08-833-823-12	Sequence 12, Appl
3	173	16.1	163	3 US-09-034-810-2	Sequence 2, Appl
4	173	16.1	163	3 US-08-085-239-2	Sequence 2, Appl
5	160.5	15.0	151	2 US-08-620-694A-8	Sequence 8, Appl
6	160.5	15.0	151	3 US-09-034-810-6	Sequence 6, Appl
7	160.5	15.0	151	3 US-09-022-255-8	Sequence 8, Appl
8	160.5	15.0	151	3 US-09-022-255-8	Sequence 8, Appl
9	160.5	15.0	151	3 US-08-085-239-6	Sequence 6, Appl
10	160.5	15.0	151	3 US-09-022-255-8	Sequence 8, Appl
11	160.5	15.0	151	3 US-09-022-260-8	Sequence 8, Appl
12	160.5	15.0	151	4 US-09-022-259-8	Sequence 8, Appl
13	160.5	15.0	151	4 US-09-022-257-8	Sequence 8, Appl
14	160.5	15.0	151	4 US-08-032-994A-4	Sequence 4, Appl
15	158	14.7	155	4 US-08-032-994A-4	Sequence 8, Appl
16	150.5	14.0	158	2 US-08-620-694A-7	Sequence 7, Appl
17	150.5	14.0	158	3 US-09-022-255-7	Sequence 7, Appl
18	150.5	14.0	158	3 US-09-022-695-7	Sequence 7, Appl
19	150.5	14.0	158	3 US-09-022-253-7	Sequence 7, Appl
20	150.5	14.0	158	3 US-09-022-260-7	Sequence 7, Appl
21	150.5	14.0	158	4 US-09-022-259-7	Sequence 7, Appl
22	150.5	14.0	158	4 US-09-022-257-7	Sequence 7, Appl
23	148.5	13.8	150	3 US-09-034-810-4	Sequence 4, Appl
24	148.5	13.8	150	3 US-08-085-239-4	Sequence 4, Appl
25	148.5	13.8	150	4 US-08-032-994A-2	Sequence 2, Appl
26	148.5	13.8	158	4 US-08-032-994A-6	Sequence 10, Appl
27	125	* 11.6	79	1 US-08-032-994A-6	Sequence 6, Appl



NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genetics Institute, Inc.  
 STREET: 87 CambridgePark Drive  
 CITY: Cambridge  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02140  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/685,239  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brown, Scott A.  
 REGISTRATION NUMBER: 32,724  
 REFERENCE/DOCKET NUMBER: G15262  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8224  
 TELEFAX: (617) 876-5851  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 163 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 LENGTH: 685-239-2

Query Match 16.1%; Score 173; DB 3; Length 163;  
 Best Local Similarity 39.0%; Pred. No. 1e-12;  
 Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

Qy 97 LEADTHQRSITSPWRYRVDTDEDRYPOKLAFAECLCRGCIDARTGRRTAAALNSVRLQLSL 156  
 Db 70 MSRNTIESRSTSPWNNTVYWDNRPYSEVQAQCRNUGCINAQ-GREDISIINSVPIQQETL 128

Qy 157 VLRRL - RPCSRDGSGLPLTPGAFAFHTEFIHPVGCTCVLP 194  
 Db 129 VVRRKHQGCS -----VSFQLEKVLVTVGCTCVTP 157

RESULT 5  
 US-08-620-694A-8  
 Sequence 8, Application US/08620694A  
 Patent No. 5889285  
 GENERAL INFORMATION:  
 APPLICANT: Yao, Zhengbin  
 SPRIGGS, Melannie  
 APPLICANT: Fanslow, William  
 TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Power Macintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5  
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/620,694A  
 FILING DATE: 21 MARCH 1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/538,765  
 FILING DATE: 7 AUGUST 1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/410,535  
 FILING DATE: 23 MARCH 1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 587-0430  
 TELEFAX: (206)  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 151 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Herpesvirus Saimiri  
 STRAIN: ORF13  
 US-08-620-694A-8

Query Match 15.0%; Score 160.5; DB 2;  
 Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
 Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

Qy 36 CYSAAEPLQGAPPHLARGKQGALPVALLYSSLEASHGRHERPSATQCPVLRPEE 95  
 Db 18 CIVKSEITSAQTPRCLAA----NNSPRSYMTLIRNWNTSSKRS----- 60

Qy 96 VLEBADTHQRSITSPWRYRVDTDEDRYPOKLAFAECLCRGCIDARTGRRTAAALNSVRLQLSL 155  
 Db 61 ---DYNRSTSPWLYRHNEDODRYPVLSIWEAKCRYLGCVNA -DGNDYDHMNSVPPQQEI 115

Qy 156 LVLRRL - RPCSRDGSGLPLTPGAFAFHTEFIHPVGCTCVLP 194  
 Db 116 LVVRKGHQCPN -----SFRLEKMLVTVGCTCVTP 145

RESULT 6  
 US-09-034-810-6  
 Sequence 6, Application US/09034810  
 Patent No. 6043344  
 GENERAL INFORMATION:  
 APPLICANT: Jacobs, Kenneth  
 APPLICANT: Kelleher, Kerry  
 APPLICANT: Carlin, McKeough  
 APPLICANT: Goldman, Samuel  
 APPLICANT: Pittman, Debra  
 APPLICANT: Mi, Sha  
 APPLICANT: Neben, Steven  
 APPLICANT: Giannotti, Joann  
 APPLICANT: Golden,Fleet, Margaret  
 APPLICANT: Golden,Fleet, Margaret  
 TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genetics Institute, Inc.  
 STREET: 87 CambridgePark Drive  
 CITY: Cambridge  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02140  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA: US/09/034.810  
 APPLICATION NUMBER: US/09/034.810  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/685,239  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brown, Scott A.  
 REGISTRATION NUMBER: 32,724  
 REFERENCE/DOCKET NUMBER: GI5262  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 498-8224  
 TELEFAX: (617) 876-5851  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 151 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-034-810-6

Query Match 15.0%; Score 160.5; DB 3; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 2.8e-11; Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;  
 Qy 36 CYSAAELPLGQAPPHLARGAKWQALPVALYSSLEAASHGRHRHERPSATTQCPVLRPEE 95  
 Db 18 CIVKSEITSAAQPRCLAA----NNSPFSRVMTLSIRNWNTSSKRAS----- 60  
 Qy 96 VLEADTHORSISPWRYRVDTDEDYPOKLAFAECLRGCCIDARTGRTETAAALNSVRLQLSL 155  
 Db 61 ---DYNRSTSPTWLTARNEQDQDRYPSVIAWEAKCRYLGCVNA-DGNYWDYHMSVPIQOEI 115  
 Qy 156 LVLR--RPCSRDGSGLPTPGAFAFHFPVGCNCVLP 194  
 Db 116 LIVRKKGHOPCPN-----SFRELKMLTVGCTCVCVP 145

RESULT 7  
 US-09-032-255-8  
 ; Sequence 8, Application US/09022255  
 ; Patent No. 6072033  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yao, Zhengbin  
 ; APPLICANT: Springs, Melanie  
 ; APPLICANT: Fanslow, William  
 ; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Power Macintosh  
 ; OPERATING SYSTEM: Apple Operating System 7.5.5  
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/022,255  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/034.810, 694  
 ; FILING DATE: 21 MARCH 1996  
 ; APPLICATION NUMBER: US/09/034.810, 694  
 ; FILING DATE: 7 AUGUST 1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/034.810, 694

APPLICATION NUMBER: US/09/034.810, 535  
 FILING DATE: 23 MARCH 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 587-0430  
 TELEFAX: (206)  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 151 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Herpesvirus Saimiri  
 STRAIN: ORF13  
 US-09-022-255-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 2.8e-11; Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;  
 Qy 36 CYSAAELPLGQAPPHLARGAKWQALPVALYSSLEAASHGRHRHERPSATTQCPVLRPEE 95  
 Db 18 CIVKSEITSAAQPRCLAA----NNSPFSRVMTLSIRNWNTSSKRAS----- 60  
 Qy 96 VLEADTHORSISPWRYRVDTDEDYPOKLAFAECLRGCCIDARTGRTETAAALNSVRLQLSL 155  
 Db 61 ---DYNRSTSPTWLTARNEQDQDRYPSVIAWEAKCRYLGCVNA-DGNYWDYHMSVPIQOEI 115  
 Qy 156 LVLR--RPCSRDGSGLPTPGAFAFHFPVGCNCVLP 194  
 Db 116 LIVRKKGHOPCPN-----SFRELKMLTVGCTCVCVP 145

RESULT 8  
 US-09-032-696-8  
 ; Sequence 8, Application US/09022696  
 ; Patent No. 6072037  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yao, Zhengbin  
 ; APPLICANT: Springs, Melanie  
 ; APPLICANT: Fanslow, William  
 ; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Power Macintosh  
 ; OPERATING SYSTEM: Apple Operating System 7.5.5  
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/022,696  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/620,694  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/034.810, 535

FILED: 23 MARCH 1995  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,695  
 REFERENCE/DOCKET NUMBER: 2617-B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 587-0430  
 TELEFAX: (206) 587-0430  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 151 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Herpesvirus Saimiri  
 STRAIN: ORF13  
 OS-09-022-696-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
 Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;  
 Query 36 CYSAAEPLGQAPPHLIARGAKWQGQALPVAVLSSLEAASHGRHERPSATTQCPVLRPEE 95  
 Db 18 CIVKSEITSAQTPRCLAA----NNSFPSRSMVNTLSTRNWNTSSKRAS----- 60

Query 96 VLEADTHQRSISPSPWYRVDTDEDYRQPKLAAECLRGCDARTGRETAAALNSVRLQLS 155  
 Db 61 ----DYNRSTSPPWTLHNRNEDDRYPSVNTLSTRNWNTSSKRAS----- 60

Query 156 LVYRR - RPCSRDGSGLPLTPGAFAAFHTEFHYPVGCTCVLP 194  
 Db 116 LVYRKGHQPCPN-----SFRLKMLVTVGCTCVTP 145

RESULT 9  
 US-08-685-239-6  
 Sequence 6, Application US/08685239  
 ; Patent No. 6074849  
 GENERAL INFORMATION:  
 ; APPLICANT: Jacobs, Kenneth  
 ; APPLICANT: Kelleher, Kerry  
 ; APPLICANT: Carlin, McKeough  
 ; APPLICANT: Goldman, Samuel  
 ; APPLICANT: Pittman, Debra  
 ; APPLICANT: Mi, Sha  
 ; APPLICANT: Nepon, Steven  
 ; APPLICANT: Giannotti, Johann  
 ; APPLICANT: Golden Fleet, Margaret  
 ; TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genetics Institute, Inc.  
 ; STREET: 87 CambridgePark Drive  
 ; CITY: Cambridge  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02140  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/685,239  
 ; FILING DATE:  
 ; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Brown, Scott A.  
 REGISTRATION NUMBER: 32,724  
 REFERENCE/DOCKET NUMBER: G15262  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 438-8224  
 TELEFAX: (617) 876-5851  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 151 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-685-239-6

Query Match 15.0%; Score 160.5; DB 3; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
 Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;  
 Query 36 CYSAAEPLGQAPPHLIARGAKWQGQALPVAVLSSLEAASHGRHERPSATTQCPVLRPEE 95  
 Db 18 CIVKSEITSAQTPRCLAA----NNSFPSRSMVNTLSTRNWNTSSKRAS----- 60

Query 96 VLEADTHQRSISPSPWYRVDTDEDYRQPKLAAECLRGCDARTGRETAAALNSVRLQLS 155  
 Db 61 ----DYNRSTSPPWTLHNRNEDDRYPSVNTLSTRNWNTSSKRAS----- 60

Query 156 LVYRR - RPCSRDGSGLPLTPGAFAAFHTEFHYPVGCTCVLP 194  
 Db 116 LVYRKGHQPCPN-----SFRLKMLVTVGCTCVTP 145

RESULT 10  
 US-09-022-253-8  
 Sequence 8, Application US/09022253  
 ; Patent No. 6096305  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Spriggs, Melanie  
 ; APPLICANT: Fanslow, William  
 ; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Power Macintosh  
 ; OPERATING SYSTEM: Apple Operating System 7.5.5  
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/022,253  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/620,694  
 ; FILING DATE: 21-MARCH-1996  
 ; APPLICATION NUMBER: US/08/538,765  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/410,535  
 ; FILING DATE: 23-MARCH-1995  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Patricia Anne  
 ; REGISTRATION NUMBER: 34,695  
 ; REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206)587-0430  
 ; TELEFAX: (206)  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 151 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: No. 6096305 Relevant  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Herpesvirus Saimiri  
 ; STRAIN: ORF13  
 US-09-022-253-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
 Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

Qy 36 CYSAAELPLGQAPPILLARGAKWGOALPVAVLSSLEAASHRGRRHERRPSATQCPVLRPEE 95  
 Db 18 CIVKSETSAAQTPRCLAA----NNSPRSNVTLSIRNWNTSSKRAS----- 60

Qy 96 VLEADTHRSISPWRYRVDTDEDRYPTOKLAFABCLCRGCIIDARTGRTAAALNSVRLQSL 155  
 Db 61 ----DYINRSTSPTWLHRNEDQDRYPSVIAWEAKCRYLGCVNA-DGNYWDHMSNSVPIQQEI 115

Qy 156 LVLRRA--RPCSRDGSGLPTPGAFAHTEFIHYPGCTCVLP 194  
 Db 116 LVRKGHOPCPN-----SFRLKMLVTVGCTCVTP 145

RESULT 11  
 US-09-022-250-8  
 ; Sequence 8, Application US/09022260  
 ; Patent No. 6100235

GENERAL INFORMATION:  
 ; APPLICANT: Yao, Zhengbin  
 ; APPLICANT: Springs, Melanie  
 ; APPLICANT: Fanslow, William  
 ; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17  
 ; NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Power Macintosh  
 ; OPERATING SYSTEM: Apple Operating System 7.5.5  
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/022,260  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/620,694  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: USSN 08/410,535  
 ; FILING DATE: 23 MARCH 1995  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Patricia Anne  
 ; REGISTRATION NUMBER: 34,695  
 ; REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206)587-0430  
 ; TELEFAX: (206)  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 151 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: not relevant  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Herpesvirus Saimiri  
 ; STRAIN: ORF13  
 US-09-022-260-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
 Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

Qy 36 CYSAAELPLGQAPPILLARGAKWGOALPVAVLSSLEAASHRGRRHERRPSATQCPVLRPEE 95  
 Db 18 CIVKSETSAAQTPRCLAA----NNSPRSNVTLSIRNWNTSSKRAS----- 60

Qy 96 VLEADTHRSISPWRYRVDTDEDRYPTOKLAFABCLCRGCIIDARTGRTAAALNSVRLQSL 155  
 Db 61 ----DYINRSTSPTWLHRNEDQDRYPSVIAWEAKCRYLGCVNA-DGNYWDHMSNSVPIQQEI 115

Qy 156 LVLRRA--RPCSRDGSGLPTPGAFAHTEFIHYPGCTCVLP 194  
 Db 116 LVRKGHOPCPN-----SFRLKMLVTVGCTCVTP 145

RESULT 12  
 US-09-022-259-8  
 ; Sequence 8, Application US/09022259  
 ; Patent No. 6191104

GENERAL INFORMATION:  
 ; APPLICANT: Yao, Zhengbin  
 ; APPLICANT: Springs, Melanie  
 ; APPLICANT: Fanslow, William  
 ; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17  
 ; NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Immunex Corporation  
 ; STREET: 51 University Street  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98101

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: Apple Power Macintosh  
 ; OPERATING SYSTEM: Apple Operating System 7.5.5  
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/022,259  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/620,694  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: USSN 08/410,535  
 ; FILING DATE: 23 MARCH 1995  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Perkins, Patricia Anne  
 ; REGISTRATION NUMBER: 34,695  
 ; REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 587-0430  
 TELEFAX: (206) 587-0430  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 151 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Herpesvirus Saimiri  
 STRAIN: ORF13  
 US-09-022-257-8

Query Match 15.0% Score 160.5; DB 4; Length 151;  
 Best Local Similarity 28.8%; Pred. No. 2.8e-11;  
 Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

Qy 36 CYSAAEPLQGAPPHLARGAKNGQALPVALVSSLEAAASHRGRHERPSATTQCPVLRPE 95  
 Db 18 CIVKSBITSQTQPRLLA-----NNSFPSQVMVTLISRWNNTSSKRAS----- 60

Qy 96 VLEADTHORSTSPWRYRVDTDEDYRQPKLALFAECLCRGGC1DARTGRETAAALNSVRLQLS 155  
 Db 61 -----DYYNRSTSPWTLHRNEDQDRYRPSV1WEAKCRYLGCVNA-DGNYDTHMNSVPIQE 115

Qy 156 LVLR-----RPSRDGGGLPPTGAGAFAHTEFHHPVNGCTCVLP 194  
 Db 116 LVVRKGHQPCPN-----SFRLERMLVTVGCTCVTP 145

RESULT 14  
 US-08-432-994A-4  
 ; Sequence 4, Application US/08432994A  
 ; Parent No. 6274711  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Golstein, Pierre  
 ; APPLICANT: Rouvier, Eric  
 ; APPLICANT: Fossiez, Francois  
 ; APPLICANT: Lebecque, Serge J.E.  
 ; APPLICANT: Djossou, Odile  
 ; APPLICANT: Banchereau, Jacques  
 ; TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-4 ANTIGENS AND  
 ; TITLE OF INVENTION: RELATED REAGENTS  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: DNAX Research Institute  
 ; STREET: 901 California Avenue  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304-1104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/432-994A  
 ; FILING DATE: 02-MAY-1995  
 ; CLASSIFICATION: 424  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/250, 846  
 ; FILING DATE: 27-MAY-1994  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/177, 747  
 ; FILING DATE: 05-JAN-1994  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/077, 203

RESULT 15

US-08-432-994A-8

Sequence 8, Application US/08432994A

Patent No. 6274711

GENERAL INFORMATION:

APPLICANT: Golstein, Pierre

APPLICANT: Rouver, Eric

APPLICANT: Fossiez, Francois

APPLICANT: Lebecque, Serge J.E.

APPLICANT: Diossou, Odile

APPLICANT: Banchereau, Jacques

TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,994A

FILING DATE: 02-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/250,846

FILING DATE: 27-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/177,747

FILING DATE: 05-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/077,203

FILING DATE: 14-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0388K3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-852-9196

TELEFAX: 415-496-1200

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 155 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-432-994A-8

Query Match 14.7%; Score 158; DB 4; Length 155;

Best Local Similarity 39.8%; Pred. No. 5.7e-11;

Matches 39; Conservative 11; Mismatches 34; Indels 14; Gaps 3;

Qy 99 ADTHQRISISPWRYRVDTDDBRYPQKLAFAECLRGCIDARTGRETAAINSVRLQQLSLVL 158

Db 64 SDYNRSTSPWNLRNEDPERPSVIAKCRHLCINA-DGNYDHYMNSVPIQQEILVL 122

Qy 159 RRRP-CSRQDGSILPTGAFAFHTEFHYPVGCTCVLP 194

Db 123 RREPHCPN-----SFRIEKILVSGCTCVP 149

Search completed: August 23, 2002, 16:01:11

Job time: 22 sec